

22910

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From: Mertz, Prema
Sent: Wednesday, August 16, 2000 9:07 AM
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Subject: 09/361,655

Please search SEQ ID NO: 12 with protein databases.

Thanks

Prema Mertz

Prema Mertz, Ph.D.

Primary Examiner

Crystal Mall 1, Room 10E01

Art Unit 1646

(703)308-4229

U.S. Patent & Trademark Office

12

Edward Hart
Technical Info Specialist
STIC / Biotech
CM1 12C14 Tel: 305-9203



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Db 292 ASFSHSAVSLKANNPMPASTSCVPTARRPISLILYLDHNGNVKTVDPMPVVEACGCS 350
 OY 61 ASFSHSAVSLKANNPMPASTSCVPTARRPISLILYLDHNGNVKTVDPMPVVEACGCS 119

RESULT 2
 ID W60619 standard; Protein: 350 AA.
 AC W60619;
 DT 01-FEB-1999 (first entry)
 DE Human liver activin beta e polypeptide.
 KW Liver activin; beta c; beta e; cell differentiation; haematopoiesis;
 KW erythroid; ovarian follicular maturation; hormone; neuronal survival;
 KW spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;
 KW osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunosassay;
 KW menstrual disorder; transgenic; modulator; human.
 OS Homo sapiens.
 PH Key
 FT Peptide 1..17 Location/Qualifiers
 FT /note="signal sequence"
 FT Domain 18..236
 FT /note="propeptide domain"
 FT Modified_site 198..200
 FT /note="Asn is putatively N-glycosylated"
 FT Cleavage_site 232..236
 FT /note="endoproteolytic cleavage site"
 FT Domain 237..350
 FT /note="mature growth factor domain"
 WO9822492-A1.
 DT 28-MAY-1998.
 PF 20-NOV-1997; US-752919.
 PR (UNMI) UNIV MICHIGAN.
 PA Bonadio U, Fang J;
 DR WPI: 98-312408/27.
 N-PSDB: V38240.
 PT New isolated nucleic acid encoding sub-units of liver activin -
 PT useful for regulating growth and differentiation of cells, e.g. for
 PT treating liver, bone and haematopoietic disorders
 PS Disclosure: Fig 5; 141pp; English.
 CC This represents a human liver activin beta e polypeptide. The invention
 CC provides murine beta c and beta e polypeptides and the encoding genes.
 CC Disorders of cell growth or differentiation (or susceptibility to them)
 CC are diagnosed by measuring liver activin gene activity or by detecting a
 CC mutation in the liver activin gene. Disorders of haematopoiesis,
 CC erythroid differentiation, ovarian follicular maturation, hormone
 CC secretion, neuronal survival, spermatogenesis, bone formation, insulin
 CC secretion or cardiac morphogenesis are some conditions that can be
 CC diagnosed using the liver activin. Cell growth and differentiation can be
 CC stimulated by treatment with an liver activin compound or agent that
 CC upregulates the compound's expression. Antagonists can be used to treat
 CC liver diseases while agonists can be used to increase growth and
 CC regeneration of liver tissue. The liver activin compound may also induce
 CC bone growth (e.g. for treating osteoporosis or osteomalacia) or
 CC haematopoiesis, particularly erythropoiesis, for treating haemophilia,
 CC cystic fibrosis or menstrual disorders. Antibodies are useful in
 CC immunosassays, to generate anti-idiotypic antibodies (which bind to liver
 CC activin receptors) and to inhibit liver activin. Also, transgenic animals
 CC containing liver activin gene can be used to produce the liver activin
 CC (in correctly processed and modified forms) proteins, or the transgenic
 CC animals, are useful for screening for liver activin modulators.
 SQ Sequence 350 AA;

Query Match 99.7%; Score 913; DB 1; Length 350;
 Best Local Similarity 99.2%; Pred. No. 2,486-87;
 Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 232 RARRPTCEPATPLCCRRDHYVDFELGWRDMLQPGYOLNCSGCPPLHAGSPGIA 291
 OY 1 RARRPTCEPATPLCCRRDHYVDFELGWRDMLQPGYOLNCSGCPPLHAGSPGIA 60
 Db 292 ASFSHSAVSLKANNPMPASTSCVPTARRPISLILYLDHNGNVKTVDPMPVVEACGCS 350
 OY 61 ASFSHSAVSLKANNPMPASTSCVPTARRPISLILYLDHNGNVKTVDPMPVVEACGCS 119

RESULT 3
 ID W60618 standard; Protein: 350 AA.
 AC W60618;
 DT 01-FEB-1999 (first entry)
 DE Murine liver activin beta e polypeptide.
 KW Liver activin; beta c; beta e; cell differentiation; haematopoiesis;
 KW erythroid; ovarian follicular maturation; hormone; neuronal survival;
 KW spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;
 KW osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunosassay;
 KW menstrual disorder; transgenic; modulator.
 OS Mus sp.
 PH Key
 FT Peptide 1..21 Location/Qualifiers
 FT /note="signal sequence"
 FT Domain 22..236
 FT /note="propeptide domain"
 FT Modified_site 198..200
 FT /note="Asn is putatively N-glycosylated"
 FT Cleavage_site 232..236
 FT /note="endoproteolytic cleavage site"
 FT Domain 237..349
 FT /note="mature growth factor domain"
 WO9822492-A1.
 DT 28-MAY-1998.
 PF 20-NOV-1997; US-752919.
 PR (UNMI) UNIV MICHIGAN.
 PA Bonadio U, Fang J;
 DR WPI: 98-312408/27.
 N-PSDB: V38238.
 PT New isolated nucleic acid encoding sub-units of liver activin -
 PT useful for regulating growth and differentiation of cells, e.g. for
 PT treating liver, bone and haematopoietic disorders
 PS Claim 16; Fig 2; 141pp; English.
 CC This represents a murine liver activin beta e polypeptide. Sequences
 CC derived from a beta c cDNA clone is used for screening and cloning the
 CC activin beta e gene. Disorders of cell growth or differentiation (or
 CC susceptibility to them) are diagnosed by measuring liver activin gene
 CC activity or by detecting a mutation in the liver activin gene. Disorders
 CC of haematopoiesis, erythroid differentiation, ovarian follicular
 CC maturation, hormone secretion, neuronal survival, spermatogenesis, bone
 CC formation, insulin secretion or cardiac morphogenesis are some conditions
 CC that can be diagnosed using the liver activin. Cell growth and
 CC differentiation can be stimulated by treatment with an liver activin
 CC compound or agent that upregulates the compound's expression. Antagonists
 CC can be used to treat liver diseases while agonists can be used to
 CC increase growth and regeneration of liver tissue. The liver activin
 CC compound may also induce bone growth (e.g. for treating osteoporosis or
 CC osteomalacia) or haematopoiesis, particularly erythropoiesis, e.g. for
 CC treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies
 CC are useful in immunosassays, to generate anti-idiotypic antibodies (which
 CC bind to liver activin receptors) and to inhibit liver activin. Also,
 CC transgenic animals containing liver activin gene can be used to produce
 CC the liver activin (in correctly processed and modified forms) proteins,
 CC or the transgenic animals, are useful for screening for liver activin
 CC modulators.
 SQ Sequence 350 AA;

Query Match 98.9%; Score 906; DB 1; Length 350;
 Best Local Similarity 97.5%; Pred. No. 1,496-86;
 Matches 116; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 232 RARRPTCEPATPLCCRRDHYVDFELGWRDMLQPGYOLNCSGCPPLHAGSPGIA 291
 OY 1 RARRPTCEPATPLCCRRDHYVDFELGWRDMLQPGYOLNCSGCPPLHAGSPGIA 60
 Db 292 ASFSHSAVSLKANNPMPASTSCVPTARRPISLILYLDHNGNVKTVDPMPVVEACGCS 350
 OY 61 ASFSHSAVSLKANNPMPASTSCVPTARRPISLILYLDHNGNVKTVDPMPVVEACGCS 119

RESULT 4

ID M60617 standard; Protein; 352 AA.

AC M60617;

DE Murine liver activin beta c polypeptide.

KM Liver activin; beta c; beta e; cell differentiation; haematopoiesis;

KW erythroid; ovarian follicular maturation; hormone; neuronal survival;

KM spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;

KW osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunosassay;

OS menstural disorder; transgenic; modulator.

MS Mus sp.

FH Key

FT Peptide

FT Modified_site

FT Modified_site

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RESULT 5

ID R89729 standard; Protein; 352 AA.

AC R89729;

DE Transforming growth factor beta MP-121.

KM TGF-beta; MP-121; mitogen; differentiation; induction; promotion;

KM maintenance; morphogen; tissue regeneration; dental implantation;

KM wound healing.

OS Homo sapiens.

FH Key

FT Protein

FT Protein

FT Protein

FT Protein

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RESULT 6

ID R10991 standard; Protein; 127 AA.

AC R10991;

DE 13-MAY-1991 (first entry)

KM Xenopus Bone Morphogenetic Factor M3.

KM BMF; osteoporosis; fracture; cartilage.

OS Xenopus laevis.

PN EP-416578-A.

PD 13-MAR-1991.

PF 05-SEP-1990; 117079.

PR 06-SEP-1989; JP-229250.

PR 20-JUL-1990; JP-190774.

PR (TAKE-) TAKEDA CHEMICAL IND KK.

PR (SCIT-) SCITECH RESEARCH CO.

PR (SCIT-) SCITECH RESEARCH CO.

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PR (SCIT-) SCITECH RESEARCH CO.

Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps

RESULT	9
ID	P70203 standard: protein: A26 AA

AC P70203;
 DT 09-APR-1991 (first entry)
 DE Sequence of human inhibin beta-chain precursor beta-A.
 KW Fertility control; contraception; hormone; spermatogenesis.
 OS Homo sapiens.
 PH Key
 FT modified_site location/Qualifiers
 FT 165..167
 FT /note="potential N-linked glycosylation sites"
 FT region 1..28
 FT /note="signal sequence"
 FT region 28..310
 FT /note="pro region"
 FT protein 311..326
 FT cleavage_site 306..310
 FT /note="proteolytic processing site"
 PN RP-222491-A.
 PR 20-MAY-1987.
 PR 02-OCT-1986; 307586.
 PR 03-OCT-1985; US-783910.
 PR 10-FEB-1986; US-827710.
 PR 12-SEP-1986; US-906729.
 PA (GETH) GENENTECH INC.
 PI Mason AJ, Seeburg PH.
 DR WPI: 87-137512/20.
 DR N-PSDB; N70315.
 PT Recombinant human or porcine inhibin or activin - used for
 PT modulating clinical condition or reproductive physiology of
 PT animals.
 PS Disclosure; Fig 8A; 48pp; English.
 CC A compen. comprising human or porcine inhibin which is completely
 CC free of unidentified or porcine proteins is claimed. Also claimed
 CC are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
 CC chain. Sequencing of inhibin-encoding cDNA has led to the
 CC identification of prodomain regions located N-terminal to the
 CC mature inhibin chains that represent coordinately expressed
 CC biologically active polypeptides. The prodomain regions or
 CC prodomain immunogens are useful in monitoring preproinhibin
 CC processing in transformant cell culture or in experiments directed
 CC at modulating the clinical cond. or reproductive physiology of
 CC animals.
 SQ Sequence 426 AA;
 Query Match 54.4%; Score 498; DB 1; Length 426;
 Best Local Similarity 45.5%; Pred. No. 1,54e-41;
 Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
 Db 306 RRRRGLECDGKVNICKKQPFVSKDIGNMDWIAPSGYHANYCEGCPSHIAGTSGSS 365
 QY 1 RARRRPTCEPATPLCCRRDHYDFQELGWRDWILOPEGYQLNVCSGCPHLAGSPGIA 60
 Db 366 LSFHSTVINHYRMGHSPPANLKSQCVPTKLRPMSTLYDDGQNIKKDIONMIVECGC 425
 QY 61 ASHSAVFS-L-LKANPMPASTSCCPTARPLSLYLHDHNGVVKTDVPMVVEACGC 118
 Db 426 S 426
 QY 119 S 119
 RESULT 10
 ID R05413 standard; protein; 426 AA.
 AC R05413;
 DT 27-JUL-1990 (first entry)
 DE BUF-3 human differentiation inducing factor gene product.
 KW BUF-3; dhfr; dihydrofolic acid reductase; differentiation.
 OS Homo sapiens.
 PN J02009388-A.
 PD 12-JAN-1990.
 PF 8-JUL-1988; 170147.
 PR 9-MAR-1988; JP-055270.
 PA (AJIN) Ajinomoto KK.
 DR WPI: 90-055348/08.
 DR N-PSDB; Q01648.

PT Physiologically active protein prepn. -
 PT by transforming plasmid having gene coding physiologically
 PT active protein and gene of dihydrofolic acid reductase to hamster
 PT ovary etc.
 PS Example 1; Fig 1; 12pp; Japanese.
 CC Gene may be expressed by transforming a dhfr negative strain of CHO cells
 CC with an active BUF-3 gene and dhfr carrying vector. BUF-3 gene product
 CC is a cell differentiating factor.
 SQ Sequence 426 AA;
 Query Match 54.4%; Score 498; DB 1; Length 426;
 Best Local Similarity 45.5%; Pred. No. 1,54e-41;
 Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;

Db 306 RRRRGLECDGKVNICKKQPFVSKDIGNMDWIAPSGYHANYCEGCPSHIAGTSGSS 365
 QY 1 RARRRPTCEPATPLCCRRDHYDFQELGWRDWILOPEGYQLNVCSGCPHLAGSPGIA 60
 Db 366 LSFHSTVINHYRMGHSPPANLKSQCVPTKLRPMSTLYDDGQNIKKDIONMIVECGC 425
 QY 61 ASHSAVFS-L-LKANPMPASTSCCPTARPLSLYLHDHNGVVKTDVPMVVEACGC 118
 Db 426 S 426
 QY 119 S 119

RESULT 11
 ID P70200 standard; protein; 427 AA.
 AC P70200;
 DT 09-APR-1991 (first entry)
 DE Sequence of porcine inhibin beta-chain precursor beta-A.
 KW Fertility control; contraception; hormone; spermatogenesis.
 OS Sus scrofa domestica.
 PH Key
 FT region location/Qualifiers
 FT 1..308
 FT /note="used to design a long synthetic DNA probe"
 FT protein 309..424
 FT cleavage_site 304..308
 FT /note="proteolytic processing site"
 PN RP-222491-A.
 PR 20-MAY-1987.
 PR 02-OCT-1986; 307586.
 PR 03-OCT-1985; US-783910.
 PR 10-FEB-1986; US-827710.
 PR 12-SEP-1986; US-906729.
 PA (GETH) GENENTECH INC.
 PI Mason AJ, Seeburg PH.
 DR WPI: 87-137512/20.
 DR N-PSDB; N70317.
 PT Recombinant human or porcine inhibin or activin - used for
 PT modulating clinical condition or reproductive physiology of
 PT animals.
 PS Disclosure; Fig 2B; 48pp; English.
 CC A compen. comprising human or porcine inhibin which is completely
 CC free of unidentified or porcine proteins is claimed. Also claimed
 CC are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
 CC chain. Sequencing of inhibin-encoding cDNA has led to the
 CC identification of prodomain regions located N-terminal to the
 CC mature inhibin chains that represent coordinately expressed
 CC biologically active polypeptides. The prodomain regions or
 CC prodomain immunogens are useful in monitoring preproinhibin
 CC processing in transformant cell culture or in experiments directed
 CC at modulating the clinical cond. or reproductive physiology of
 CC animals.
 SQ Sequence 427 AA;
 Query Match 54.4%; Score 498; DB 1; Length 427;
 Best Local Similarity 45.5%; Pred. No. 1,54e-41;
 Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;

Db 307 RRRRGLECDGKVNICKKQPFVSKDIGNMDWIAPSGYHANYCEGCPSHIAGTSGSS 366
 QY 1 RARRRPTCEPATPLCCRRDHYDFQELGWRDWILOPEGYQLNVCSGCPHLAGSPGIA 60
 Db 426 S 426
 QY 119 S 119

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QY      1 RAARRRPTCEPATPLCCRRDHVYFOELGWRDMTLOPEGYQLWCSCGCPPLIAGSPGIA 60
Dbo    367 LSEHSTVYNHYMRGSHSPANILKSCCVPTKLPRMSMLYYDDGONITKKIDQMITYEECGC 426
      61 ASPHSANVFS-L-KANNPMPASTSCCVPTARRPLSLILYIDHNGNMYKTDVPMNVEAAGC 118
Dbo    427 S 427
QY      119 S 119

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ID RESULT 12
 AC R10990 standard; Protein; 130 AA.
 AC R10990;
 DT 13-MAY-1991 (first entry)
 DE Xenopus Bone Morphogenetic Factor B9.
 KW BMF; osteoporosis; fracture; cartilage.
 OS Xenopus laevis.
 PN EP-416578-A.
 PS
 PD 13-MAR-1991.
 PF 05-SEP-1990; 117079.
 06-SEP-1988; JP-229250.
 20-JUL-1990; JP-190774.
 (TAKE) TAKEDA CHEMICAL IND KK.
 PI (SCIT-) SCITECH RESEARCH CO.
 PI Murakami K, Ikeno N, Kato Y;
 DR WPI: 91-075112/11.
 DR N-PSDB: Q10890.
 PT Xenopus laevis bone morphogenetic protein and DNA encoding it -
 PT used in therapy of fracture or osteoporosis
 PS Claim 2: Fig 3; 28pp; English.
 PS A Xenopus laevis liver-derived DNA library in Charon 28 vector, was
 screened with a rat activin beta-A cDNA probe. Five clones were
 CC identified, including clone B9. They were subcloned in pUC19 and used
 CC to transform competent E. coli HB101 cells. Transformant E. coli HB101/
 CC pXa9 coding for the B9 BMP was sequenced and the amino acid
 CC sequence of B9 deduced from it.
 CC See also Q10891-7.
 Q0 Sequence 130 AA;

RESULT	13
ID	R12088 standard; Protein; 116 AA.
AC	R12088;
DT	01-AUG-1991 (first entry)
DE	16.5 kD subunit of ovine inhibin
KW	Follicle stimulating hormone; FSH; luteinizing hormone; LH;
KW	fertility; gonadotropin.
OS	Crambe abyssinica.
PN	U55015729-A.
PD	14-MAY-1991.
PF	23-JUN-1988; 210683.
PR	24-JUN-1986; US-678063.
PR	23-JUN-1988; US-210683.
PA	(SALK) SALK INST FOR BIOL STUD.
PI	Solness J, Rivier JEF, Bardin CW, Vale WW;
WR	WEL: 91-169615/22.

PT Pure ovine inhibin protein - which inhibits secretion of follicle
 stimulating hormone while not inhibiting secretion of lutealising
 PT hormone.
 PS Claim 1, Page 11, 11pp, English.
 CC The sequence is the N-terminal of the 16.5 kD subunit of the ovine
 CC inhibin dimer. The protein specifically inhibits basal secretion of
 CC follicle stimulating hormone (FSH) but not that of lutealising
 CC hormone (LH). It can be admin. to mammals for control of fertility,
 CC gonadotrophin secretion or sex hormone prodn. Admin decreases
 CC fertility in females and decreases spermatogenesis in males. The
 CC protein can also be used to diagnose infertility. Antibodies raised
 CC against the protein acn neutralise the activity and could be used in
 CC immunisation to block endogenous secretion of inhibin, elevating
 CC endogenous gonadotrophin secretion. The protein was purified from
 CC ram rete testis fluid by a combination of gel filtration and
 CC reverse phase HPLC. See also R12087.
 SO Sequence 116 AA.

ID RESULT 14
 AC R26481; standard; peptide; 116 AA.
 DT R26481;
 DE 02-MAR-1993 (first entry)
 DE Activin-like peptide.
 KW Anti-activin antibody; diagnosis; megakaryocyte thrombocytopaenia.
 PS Synthetic.
 PN J04323461-A.
 PD 20-AUG-1992.
 PF 28-DEC-1990; 409591
 PR 28-DEC-1990; JP-409591.
 PR (MOCH) MOCHIDA PHARM CO LTD.
 RA WPI; 92-327039/40.
 PT Determination of activin using anti-activin antibody - for the
 PT diagnosis of megakaryocyte thrombocytopaenia
 PS Disclosure; Page 16; 18pp; Japanese.
 CC The peptide shown is an activin-like peptide which was used to
 CC demonstrate a method of detecting activin and/or an activin-like
 CC substance using an antibody recognising all or part of activin. The
 CC method comprises an enzyme immunoassay, RIA, chemilumino-assay,
 CC fluoro-immunoassay or time resolved fluorescence immunoassay using
 CC the index of coagulation of latex grain to erythrocyte. The
 CC measurement of activin and/or activin-like substance is useful for
 CC the diagnosis of megakaryocyte thrombocytopaenia.
 CC See also R26480-2.
 CC Sequence 116 AA;

RESULT	15
ID	P80019 standard; Protein; 116 AA.

Release 3.1A John F. Collins, Biocomputing Research Unit
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Tabular output not generated.

Sequence:

Searched:

Database:

Statistics:

and is

SUMMARIES

Alt. No.	Score	Match	Query Length	DB	ID	Description	Pred. No.
1	906	98.9	350	2	JC5241	activin beta E chain	8.86e-200
2	902	98.9	352	2	JC5080	activin beta C precursor	5.41e-122
3	629	68.7	352	2	JC5366	activin beta C - mos	3.16e-122
4	619	67.6	367	2	JC4151	activin beta D chain	1.13e-122
5	616	67.6	352	2	JC2467	inhibin beta C chain	6.59e-122
6	503	54.9	425	2	I47072	inhibin beta-A chain	2.83e-96
7	498	54.4	424	1	WFPGBA	inhibin beta-A chain	5.11e-95
8	498	54.4	424	1	S31440	inhibin beta-A chain	5.11e-95
9	498	54.4	425	1	B52088	inhibin beta-A chain	5.11e-95
10	498	54.4	426	1	B24282	inhibin beta-A chain	5.11e-95
11	487	53.2	424	1	B40905	inhibin beta-A chain	2.95e-92
12	474	51.7	370	2	I51199	activin beta B subunit	5.30e-88
13	472	51.5	413	2	JC4862	activin beta-A chain	1.68e-88
14	471	51.4	255	2	I48283	inhibin beta-B chain	2.98e-88
15	471	51.4	411	2	B41398	inhibin beta-B chain	2.98e-88
16	468	51.1	349	1	WFPGBB	inhibin beta-B chain	1.68e-87
17	468	51.1	407	1	AA0150	inhibin beta-B chain	1.68e-87
18	468	51.1	408	2	S50899	betab inhibin precurs	1.67e-86
19	464	50.7	393	2	PM0103	activin beta B - zebr	5.06e-81
20	442	48.3	115	2	PM0506	activin beta B-2 chain	8.97e-81
21	441	48.1	115	2	PM0505	activin beta B-1 chain	1.57e-79
22	436	47.6	115	2	PM0504	inhibin beta A chain	4.00e-71
23	402	43.9	102	2	A65192	inhibin beta-A chain	

24	388	42.4	101	2	C36192	inhibin beta-B2 chain	1.10e-67
25	386	42.1	101	2	E36192	inhibin beta-B1 chain	3.42e-67
26	355	38.8	398	2	JH0688	bone morphogenetic pr	1.26e-59
27	355	38.8	398	2	JH0687	bone morphogenetic pr	1.26e-59
28	352	38.4	400	2	A49147	bone morphogenetic pr	6.72e-59
29	352	38.4	401	2	JH0689	bone morphogenetic pr	6.72e-59
30	352	38.4	408	2	S58791	bone morphogenetic pr	6.72e-59
31	352	38.4	408	2	S38343	bone morphogenetic pr	6.72e-59
32	352	38.4	408	1	BMH4	bone morphogenetic pr	6.72e-59
33	352	38.4	420	2	I49541	bone morphogenetic pr	1.17e-58
34	351	38.3	405	2	I50608	bone morphogenetic pr	2.05e-58
35	350	38.2	393	2	S37073	bone morphogenetic pr	2.05e-58
36	350	38.2	394	2	S45355	bone morphogenetic pr	2.05e-58
37	350	38.2	396	1	BMH325	bone morphogenetic pr	1.91e-57
38	346	37.8	353	2	I50607	bone morphogenetic pr	3.10e-56
39	341	37.2	372	2	C39364	GDF-1 embryonic growt	9.42e-56
40	339	37.0	408	2	JH0801	bone morphogenetic pr	2.66e-54
41	333	36.4	373	2	PW0042	activin - fruit fly (8.00e-54
42	331	36.1	360	2	A29619	Vg1 embryonic growth	8.00e-54
43	331	36.1	513	1	BMH05	bone morphogenetic pr	8.00e-54
44	327	35.7	207	2	S37618	vgr protein - rat (fr	7.34e-53
45	327	35.7	510	2	A47958	Vg1-related protein	7.34e-53

ALIGNMENTS

ENTRY	RESULT	1
JC5241	#type complete	
activin beta E	chain precursor	- mouse
#formal_name	Mus musculus	#common_name mouse
25-Apr-1997	#sequence-revision	09-May-1997 #text-change
DATE		

ACCESSIONS	JC5241; JC5367
REFERENCE	JC5241

#journal	#title
Biochem. Biophys. Res. Commun. (1996) 228:669-674	Molecular cloning of the mouse activin beta E subunit gene

```
#Cross-references MUID:9/096313
#Contents      liver
#accession     JC5241
```

```

#Residues      1-350  ##label  FAN
#Cross-references GB:U96386; NID:g2072521; PID:g2072522
REFERENCE      JC5366

```

#authors Fang, J., Wang, S., Smiley, E., Bonaldo, A.
#journal Biochem. Biophys. Res. Commun. (1997) 231:655-661
#title Genes coding for mouse activin beta C and beta E are closely
linked and exhibit a liver-specific expression pattern in

adult tissues.
#cross-references MUID:97224404
#accession JCS367

```

#molecule_type DNA
#residues 1-350 ##label FA2
#cross-references GB:U96386; NID:g2072521; PID:g2072522
#comment This protein is a member of the transforming growth factor-beta

```

COMMENT superfamily. There are three activins, A, B, and AB consisting of different combination of beta subunits. Activin beta C and beta E form a distinct subset of related

GENETICS acclivus.
#introns 99/3
CISACTINATION #superfamily inhibin

SUMMARY	#length 350	#molecular-weight 39057	#checksum 2625
Query Match	98.9%	Score 906;	DB 2: Length 350;

333 RARPTCTCFPTPTLCCRRDHYVDFOELGWRDWILOPEGYOLNYCGCCPPLAGSPGIA
 Best Loca Similarity 31.5%, Rec. No. 0.00 20%
 Matches 116; Conservative 2; Mismatches 1; Indels 0; Gap

1 RARRRTPTCEPATFLCCRRDHYVDPEQELGWRDWILQPEGYQLNYCSGGCPHLAGSPGIA 60

##experimental source liver
COMMENT This protein is a member of the TGF-beta superfamily, activins
compose of homo or heterodimers of the beta A and beta B chain.

GENETICS
#gene GDB:INHBC
##cross-references GDB:632884

CLASSIFICATION
#map_position 2cen-2q13
#superfamily inhibin
KEYWORDS
glycoprotein

FEATURES
1-18 #domain signal sequence #status predicted #label SIG
19-236 #domain propeptide #status predicted #label PRO
237-352 #product activin beta C #status predicted #label MAT
110,143,161 #binding_site carbohydrate (asn) (covalent) #status
predicted

SUMMARY
#length 352 #molecular-weight 38238 #checksum 8314

Query Match 67.2%; Score 616; DB 2; Length 352;
Best Local Similarity 63.9%; Pred. No. 6,596-125;
Matches 76; Conservative 26; Mismatches 15; Indels 2; Gaps 2;

Db 234 HRRGIDCGGSMCCRGFFVFRRTGHWDTIOPEGAMNFCIGCCPLHAGMPGTAAS 293
QY 3 RRRPTCEPATPLCCRRDHYVDFDELGWRDWLOPEGGYQLNCSGQCPHLAGSPGTAAS 62

Db 294 FHTAVLNLEKATAGTTGGGSCVPTARRPLSLHYDRDSNIVYTDIDPMVAVACGCS 352
QY 63 FHSAYVSLKANNPW-PAST-SCVPTARRPLSLYLDHNGNVVKTDPDMVAVACGCS 119

RESULT 6
ENTRY 147072 #type complete
TITLE Inhibin beta-A chain precursor - sheep
ORGANISM #formal_name Ovis orientalis aries, Ovis ammon aries
#common_name domestic sheep
DATE 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change
16-Jul-1999

ACCESSIONS
147072
147072: B60856

REFERENCE
#authors Fleming, J.S.; Gallowsay, S.M.; Crawford, R.J.; Tisdall, D.J.;
Greenwood, P.J.
#journal Mol. Reprod. Dev. (1995) 40:1-8
#title Tissue-specific variation in the length of the 5'
untranslated region of the beta A-inhibin mRNA in sheep.
#cross-references MIM:95217464
#accession 147072
#status preliminary; translated from GB/EMBL/DBJ

SUMMARY
#molecule_type mRNA
#residues 1-425 #label FLE
##cross-references GB:L19218; NID:g110379; PIDN:AA041621.1; PID:g310380
A60856

REFERENCE
#authors Leversha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.;
Hearn, M.T.W.; Wettenthal, R.E.H.; Findlay, J.K.; Burger,
H.G.; de Kretser, D.M.
#journal J. Endocrinol. (1987) 113:213-221
#title Isolation of inhibin from ovine follicular fluid.
#cross-references MIM:87224684
#accession B60856

COMMENT
#molecule_type protein
#residues 310-312, 'X', 314-319, 'XX', 322 #label LEV
COMMENT Inhibin suppresses follicle-stimulating hormone secretion.
CLASSIFICATION
#superfamily inhibin
KEYWORDS
disulfide bond; glycoprotein; gonad; heterodimer; hormone
SUMMARY
#length 425 #molecular-weight 47565 #checksum 2083

Query Match 54.9%; Score 503; DB 2; Length 425;
Best Local Similarity 46.3%; Pred. No. 2,836-96;
Matches 56; Conservative 31; Mismatches 32; Indels 2; Gaps 2;

Db 305 RRRRGLEDGKVNICKCKQFYVFKDIGNWMIAPSGYHANYCEGCPHLAGTSGSS 364
QY 1 RARRRPTCEPATPLCCRRDHYVDFDELGWRDWLOPEGGYQLNCSGQCPHLAGSPGTA 60

Db 365 LSFHSTVINHYRMGRHSFANLKSCVPTKLRPMSTMITYDDGQNIKKDQNNIVECCG 424
QY 61 ASFHSAVPS-L-LKANNPWPASTSCVPTARRPLSLYLDHNGNVVKTDPDMVAVACG 118

Db 425 S 425
QY 119 S 119

RESULT 7
ENTRY WEPGBA #type complete
TITLE inhibin beta-A chain precursor - pig
ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig
DATE 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change
18-Jun-1999

ACCESSIONS
A01393
A93371

REFERENCE
#authors Mason, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.;
Ying, S.Y.; Guillemin, R.; Miall, H.; Seeburg, P.H.
#journal Nature (1985) 318:659-663
#title Complementary DNA sequences of ovarian follicular fluid
inhibin show precursor structure and homology with
transforming growth factor-beta.
#cross-references MIM:86092207
#accession A01393

COMMENT
#molecule_type mRNA
#residues 1-424 #label MAS
##cross-references GB:X03266; NID:92002; PIDN:CAA27020.1; PID:g2003

COMMENT
The source of this protein is ovarian follicular fluid.
The mature protein is the carboxyl-terminal segment of a precursor
polypeptide; the active molecule is a dimer of one beta and one
alpha chain, linked by one or more disulfide bonds. Two different
forms of inhibin have been isolated (A and B) that differ in the
amino-terminal sequence of their beta chains.
Inhibin is secreted by ovaries or testes and inhibits the secretion
of follicleotropin by the pituitary gland.
#superfamily inhibin
CLASSIFICATION
#domain signal sequence #status predicted #label SIG
#domain propeptide #status predicted #label PRO
#product inhibin beta-A chain #status predicted #label
MAT

KEYWORDS
1-20
21-308
309-424

165
#binding_site carbohydrate (asn) (covalent) #status
predicted

SUMMARY
#length 424 #molecular-weight 47476 #checksum 1246

Query Match 54.4%; Score 498; DB 1; Length 424;
Best Local Similarity 45.5%; Pred. No. 5,116-95;
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;

Db 304 RRRRGLEDGKVNICKCKQFYVFKDIGNWMIAPSGYHANYCEGCPHLAGTSGSS 363
QY 1 RARRRPTCEPATPLCCRRDHYVDFDELGWRDWLOPEGGYQLNCSGQCPHLAGSPGTA 60

Db 364 LSFHSTVINHYRMGRHSFANLKSCVPTKLRPMSTMITYDDGQNIKKDQNNIVECCG 423
QY 61 ASFHSAVPS-L-LKANNPWPASTSCVPTARRPLSLYLDHNGNVVKTDPDMVAVACG 118

Db 424 S 424
QY 119 S 119

RESULT 8
ENTRY S31440 #type complete
TITLE inhibin beta-A chain - mouse
ALTERNATE_NAMES
activin A; mesoderm-inducing factor WEHI-MIF
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
10-Sep-1999

ACCESSIONS
A60087; I48265; S31440
A60087

#authors Albano, R.M.; Godsave, S.F.; Huylebroeck, D.; Van Nimmen, K.;
#journal Isaacs, H.V.; Slack, J.M.W.; Smith, J.C.
#title Development (1990) 110:435-443
#cross-references EMBL:110435-443
#accession A60087
#molecule-type protein
#residues 309-311, 'X', 313-318, 'XX', 321-325 ##label AL2
#REFERENCE 148243
#authors Albano, R.M.; Groome, N.; Smith, J.C.
#journal Development (1993) 117:711-723
#title Activins are expressed in preimplantation mouse embryos and
in ES and EC cells and are regulated on their
differentiation.
#cross-references MUID:93321614
#accession I48265
#status Preliminary; translated from GB/EMBL/DDAY
#molecule-type mRNA
#residues 1-424 ##label RES
#cross-references EMBL:X69619; NID:950145; PIDN:CAA9325.1; FID:950146
#APPLICATION #superfamily inhibin
#length 424 #molecular-weight 47392 #checksum 2136
SUMMARY
Query Match 54.4%; Score 498; DB 1; Length 424;
Best Local Similarity 45.5%; Pred. No. 5,11e-95;
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
DB 304 RRRRGLEDCKGVNICKKQFVSKDIGNMDITAPSGYHANYCEGCPHSIAGTSSGS 363
OY 1 RARRRTPCEPATPLCCRDHYDFDELGWRMDLLOPEGLYVCGGCPHLAGSGIA 60
DB 364 LSFHSTVINHYRMGRHSPFANKSCVPTKLRPMMLYYDDGQNIIRKIDQNIATVECCG 423
OY 61 ASFSHSAVFS-L-LKANNPWPASTSCVPTARRPISLTLYLDHNGNVKTDVDPVVEACGC 118
DB 424 S 424
OY 119 S 119
RESULT 9
ENTRY #type complete
TITLE inhibin beta-A chain precursor - bovine
ALTERNATE_NAMES activin; mesoderm inducing factor
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
#cross-references EMBL:1016238
#accession S50898
#molecule-type DNA
#status Preliminary
#residues 1-425 ##label THO
#cross-references EMBL:016238
#REFERENCE A94097
#authors Forage, R.G.; Ring, J.M.; Brown, R.M.; McInerney, B.V.;
Cobon, G.S.; Gregson, R.P.; Robertson, D.M.; Morgan, F.J.;
Hearn, M.T.W.; Findlay, J.K.; Wettenhall, R.E.H.; Burger,
H.G.; De Kretser, D.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:3091-3095
#title Cloning and sequence analysis of cDNA species coding for the
two subunits of inhibin from bovine follicular fluid.
#cross-references MUID:86205842
#accession B25732
#molecule-type mRNA
##status

##residues 258-425 ##label FOR
#cross-references GB:M13774; NID:9163196; PIDN:AAA97415.1; PID:9163197
#note part of this sequence, including the amino end of the
mature protein, was confirmed by protein sequencing
#REFERENCE A60960
#authors Chertov, O.Y.; Krasnosel'skii, A.L.; Bogdanov, M.F.;
#journal Hoperskaya, O.A.
#title Biomed. Sci. (1990) 1:499-506
#title Mesoderm-inducing factor from bovine amniotic fluid:
purification and N-terminal amino acid sequence
determination.
#cross-references MUID:92126853
#accession A60960
#molecule-type protein
#residues 310-312, 'X', 314-319, 'XX', 322-328, 'P' ##label CHE
#REFERENCE A61548
#authors Fukuda, M.; Miyamoto, K.; Hasegawa, Y.; Nomura, M.; Igarashi,
M.; Kangawa, K.; Matsuo, H.
#journal Mol. Cell. Endocrinol. (1986) 44:55-60
#title Isolation of bovine follicular fluid inhibin of about 32 kDa.
#cross-references MUID:86136989
#accession B61548
#molecule-type protein
#residues 310-313 ##label FUK
GENETICS
#introns 130/1
CLASSIFICATION #superfamily inhibin
KEYWORDS disulfide bond; glycoprotein; gonad; heterodimer; homodimer;
hormone
FEATURE
1-28 #domain signal sequence #status predicted #label SIG\
29-309 #product beta-A inhibin/activin #status experimental
310-425 #label MAT\
165 #binding site carbohydrate (asn) (covalent) #status
predicted
SUMMARY
#length 425 #molecular-weight 47321 #checksum 988
Query Match 54.4%; Score 498; DB 1; Length 425;
Best Local Similarity 45.5%; Pred. No. 5,11e-95;
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
DB 305 RRRRGLEDCKGVNICKKQFVSKDIGNMDITAPSGYHANYCEGCPHSIAGTSSGS 364
OY 1 RARRRTPCEPATPLCCRDHYDFDELGWRMDLLOPEGLYVCGGCPHLAGSGIA 60
DB 365 LSFHSTVINHYRMGRHSPFANKSCVPTKLRPMMLYYDDGQNIIRKIDQNIATVECCG 424
OY 61 ASFSHSAVFS-L-LKANNPWPASTSCVPTARRPISLTLYLDHNGNVKTDVDPVVEACGC 118
DB 425 S 425
OY 119 S 119
RESULT 10
ENTRY #type complete
TITLE inhibin beta-A chain precursor - human
ALTERNATE_NAMES activin A; activin AB chain A; erythroid differentiation
factor; megakaryocyte differentiation active protein
ORGANISM #formal_name Homo sapiens #common_name man
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
#cross-references EMBL:330488; B23556; B24248; A30884; S33351; PND010
#accession S30488
#REFERENCE S30488
#authors Raimondo, K.; Handa, S.I.; Ueno, N.; Murakami, K.; Fukamizu,
A.
#journal DNA Seq. (1991) 2:103-110
#title Structure and sequence analysis of the human activin beta(A)
subunit gene.
#cross-references MUID:92135888
#accession S30488
#status Preliminary

```

##molecule-type DNA
##residues 1-426 ##label TAN
##cross-references EMBL:X57578; NID:g28351; PIDN:CAA40805.1; PID:g825621
##note the authors translated the codon GAG for residue 53 as
Gly and GAG for residue 56 as Gly
REFERENCE
#authors A91366
Stewart, A.G.; Milborrow, H.M.; Ring, J.M.; Crowther, C.E.;
Forge, R.G.
#journal FEBS Lett. (1986) 206:329-334
#title Human inhibin genes. Genomic characterisation and sequencing.
#cross-references NID:87005283
#accession B23556
##molecule-type DNA
##residues 311-426 ##label STE
##cross-references GB:X04447; NID:g33928; PIDN:CAA2804.1; PID:g33929
REFERENCE
#authors A90123
Mason, A.J.; Niall, H.D.; Seeburg, P.H.
#journal Biochem. Biophys. Res. Commun. (1986) 135:957-964
#title Structure of two human ovarian inhibins.
#cross-references NID:86186863
#accession B24248
##molecule-type mRNA
##residues 1-426 ##label MAS
##cross-references GB:M13436; NID:g186414; PIDN:AA59168.1; PID:g307069
REFERENCE
#authors A30884
Murata, M.; Eto, Y.; Shibai, H.; Sakai, M.; Muramatsu, M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1988) 85:2434-2438
#title Erythroid differentiation factor is encoded by the same mRNA
as that of the inhibin beta-A chain.
#cross-references NID:88190086
#accession A30884
##molecule-type mRNA
##residues 1-426 ##label MUR
##cross-references GB:J03634; NID:g181946; PIDN:AA35787.1; PID:g181947
REFERENCE
#authors S33351
Berg, H.; Walter, M.; Northemann, W.
#submission Submitted to the EMBL Data Library, April 1993
#description Nucleotide sequence coding for the mature subunit beta(A) of
human inhibin in testis.
#accession S33351
##status preliminary
##molecule-type mRNA
##residues 311-376, 'AC', 380-426 ##label BER
##cross-references EMBL:X72498; NID:g297786; PIDN:CAA51163.1;
PID:g755740
REFERENCE
#authors PND010
Fujimoto, K.; Kawakita, M.; Kato, K.; Yonemura, Y.; Masuda,
T.; Matsuzaki, H.; Hirose, J.; Isaji, M.; Sasaki, H.;
Inoue, T.; Takatsuki, K.
#journal Biochem. Biophys. Res. Commun. (1991) 174:1163-1168
#title Purification of megakaryocyte differentiation activity from a
human fibrous histiocyte cell line: N-terminal sequence
homology with activin A.
#cross-references NID:91144591
#accession PND010
##molecule-type protein
##residues 311-313, 'X', 315-320, 'XX', 323-328, 'X', 330-334 ##label FUJ
COMMENT Activins A and B are homodimers of inhibin beta-A or inhibin
beta-B, respectively, while activin AB is a heterodimer. Inhibins
A and B are heterodimers of the inhibin alpha chain with inhibin
beta-A and beta-B, respectively.
GENETICS
#genes GDB:IMHBA
#cross-references GDB:119346; OMIM:147290
#map_position 7p15-7p13
#introns 129/3
CLASSIFICATION #superfamily inhibin
#keywords glycoprotein; gonad; heterodimer; homodimer; hormone
FEATURE
#domain signal sequence #status predicted #label SIG\
1-28
#domain propeptide #status predicted #label PRO\
29-310
#product inhibin beta A chain #status experimental
#label MAT\
311-426

```

```

165 #binding site carbohydrate (Asn) (covalent) #status
SUMMARY #length 426 #molecular-weight 47442 #checksum 3853
Query Match 54.4%; Score 498; DB 1; Length 426;
Best local similarity 45.5%; Pred. No. 5,11e-95;
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
Db 306 RRRRGLEDCGKYNICKCKKQFFVSFKDIGMNDWIAPSGYANACEGCSHIAITSGSS 365
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
1 RARRPTCEPATPLCCRDHYDFOELGMDWILQPGYOLNCSQCPHLAGSPGTA 60
Db 366 LSFSTVINYHNRGHSPPANIKSCCVPTKLPMSTMLYDDGNIIRKDIQNNIVECCG 425
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
61 ASFSHSAVES-L-LKANNPWPASTSCVPTARRPPLSLYLDHNGNVKTDVDMVEACCG 118
Db 426 S 426
|
Qy 119 S 119
RESULT 11
ENTRY B40905 #type complete
TITLE Inhibin beta-A chain precursor - rat
ORGANISM Rattus norvegicus #common_name Norway rat
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
10-Sep-1999
ACCESSIONS B40905; B40056
REFERENCE
#authors Esch, F.S.; Shimasaki, S.; Cocksey, K.; Mercado, M.; Mason,
A.J.; Ying, S.Y.; Ueno, N.; Ling, N.
#journal Mol. Endocrinol. (1987) 1:388-396
#title Complementary deoxyribonucleic acid (cDNA) cloning and DNA
sequence analysis of rat ovarian inhibins.
#cross-references NID:90331931
#accession B40905
##status preliminary; not compared with conceptual translation
##molecule-type mRNA
##residues 1-424 ##label ESC
#authors Woodruff, T.K.; Meunier, H.; Jones, P.B.C.; Hsueh, A.J.W.;
Mayo, K.E.
#journal Mol. Endocrinol. (1987) 1:561-568
#title Rat inhibin: molecular cloning of alpha- and beta-subunit
complementary deoxyribonucleic acids and expression in the
ovary.
#cross-references NID:91042598
#accession B40056
##status preliminary
##molecule-type mRNA
##residues 1-366, 'H', 368-424 ##label WOO
##cross-references GB:X7482; NID:g204936; PIDN:AAA41436.1; PID:g204937
CLASSIFICATION #superfamily inhibin
SUMMARY #length 424 #molecular-weight 47356 #checksum 1734
Query Match 53.2%; Score 487; DB 1; Length 424;
Best local similarity 44.6%; Pred. No. 2,95e-92;
Matches 54; Conservative 32; Mismatches 33; Indels 2; Gaps 2;
Db 304 RRRRGLEDCGKYNICKCKKQFFVSFKDIGMNDWIAPSGYANACEGCSHIAITSGSS 363
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
1 RARRPTCEPATPLCCRDHYDFOELGMDWILQPGYOLNCSQCPHLAGSPGTA 60
Db 364 LSFSTVINYHNRGHSPPANIKSCCVPTKLPMSTMLYDDGNIIRKDIQNNIVECCG 423
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
61 ASFSHSAVES-L-LKANNPWPASTSCVPTARRPPLSLYLDHNGNVKTDVDMVEACCG 118
Db 424 S 424
|
Qy 119 S 119
RESULT 12

```

Db	413 S 413	119 S 119
RESULT	14	
ENTRY	I48235	
TITLE	Inhibin beta-B chain - mouse (fragment)	
ALTERNATE_NAMES	activin bd chain	
ORGANISM	#normal_name Mus musculus #common_name house mouse	
DATE	02-Jul-1996 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999	
ACCESSIONS	I48235; I48256; S31441	
REFERENCE	I48235	
#authors	Ritvos, O.; Gilbert, T.; Eramaa, M.; Salnio, K.; Hilden, K.; Saxen, L.; Thibert, S.F.	
#journal	Mech. Dev. (1995) 50:229-245	
#title	Activin disrupts epithelial branching morphogenesis in developing glandular organs of the mouse.	
#cross-references	EMBL:95344997	
#accession	I48235	
##status	preliminary; translated from GB/EMBL/DBJ	
##molecule_type	mrna	
##residues	1-234 #label RES	
##cross-references	EMBL:X83376; NID:g603571; PIDN:CAAS8290.1; PID:g603572	
REFERENCE	I48243	
#authors	Albano, R.M.; Grome, N.; Smith, J.C.	
#journal	Development (1993) 117:711-723	
#title	Activins are expressed in preimplantation mouse embryos and in ES and EC cells and are regulated on their differentiation.	
#cross-references	EMBL:93321614	
#accession	I48266	
##status	preliminary; translated from GB/EMBL/DBJ	
##molecule_type	mrna	
##residues	134, 'D', 136-225 #label AUB	
##cross-references	EMBL:569620; NID:g50147; PIDN:CAAA9326.1; PID:g50148	
CLASSIFICATION	#superfamily Inhibin	
SUMMARY	#length 235 #checksum 6134	
Query Match	51.4%; Score 471; DB 2; Length 255;	
Best Local Similarity	48.3%; Pred. No. 2,98e-88;	
Matches	58; Conservative 27; Mismatches 34; Indels 1; Gaps 1;	
Db	136 RIKRRLGEGDGTSTCCROPFIDFRLLGDMIIAPGYGYNCEGSCPAYLAGVGS4 195	
Oy	1 RARRRPFCEPPTPLCCRRHDYVDFQGLGRBMDLLOPEYQLNCSQCCPHLAGSPG14 60	
Db	196 SSTRHVAIVQYMRGLNGPYNSSCIPYTKLSSMSMLYFDDEENIYKRDYPRMIVEECG4 255	
Oy	61 ASHSASVFSLKANNPWAST-SCCVFTARPLSLIYLDHNSNVKTDVDPNVAEAGCS 119	
RESULT	15	
ENTRY	B41398	
TITLE	Inhibin beta-B chain precursor - rat	
ALTERNATE_NAMES	Inhibin/activin beta B-chain	
ORGANISM	#normal_name Rattus norvegicus #common_name Norway rat	
DATE	03-Apr-1992 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999	
ACCESSIONS	B41398; I53286; C40905	
REFERENCE	B41398	
#authors	Feng, Z.M.; Li, Y.P.; Chen, C.T.C.	
#journal	Mol. Endocrinol. (1989) 3:1914-1925	
#title	Analysis of the 5'-flanking regions of rat inhibin alpha-beta-g-subunit genes suggests two different regulatory mechanisms.	
#cross-references	MUJID:90190649	
#accession	B41398	
##status	preliminary	
##molecule_type	DNA	


```

##residues      1-174 ##label FEN
##cross-references GB:M32755; GB:M32757; NID:g204963; PIDN:AAA4138.1;
PID:g554460

REFERENCE
#authors      Dykema, J.C.; Mayo, K.E.
#journal      Endocrinology (1994) 135:702-711
#title        Two messenger ribonucleic acids encoding the common beta
              B-chain of inhibin and activin have distinct 5'-initiation
              sites and are differentially regulated in rat granulosa
              cells.
#cross-references MUID:94307180
#accession    I53288
#status       Preliminary; translated from GB/EMBL/DDBJ
#molecule_type DNA
#residues     1-7 #label RES
#cross-references GB:S72477; NID:g619268
A40905
#authors      Esch, F.S.; Shimozaki, S.; Cooksey, K.; Mercado, M.; Mason,
              A.J.; Ying, S.Y.; Ueno, N.; Ling, N.
#journal      Mol. Endocrinol. (1987) 1:388-396
#title        Complementary deoxyribonucleic acid (cDNA) cloning and DNA
              sequence analysis of rat ovarian inhibins.
#cross-references MUID:90331931
#accession    C40905
#status       Preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues     133-411 #label ESC
CLASSIFICATION #superfamily inhibin
SUMMARY        #length 411 #molecular-weight 45182 #checksum 2167

Query Match          51.4%; Score 471; DB 2; Length 411;
Best Local Similarity 48.3%; Pred. No.2,98e-88;
Matches             58; Conservative         27; Mismatches 34; Indels 1; Gaps 1;

Db   292 RIRKRGLECDGRTSLCCNQGFDFRFLIGMWDIITAPGYGNCTCSCRAYLAGVGSA 351
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QY   1 RARRPTPCCEATPLCCRDRHYDFOELGWMDWLOPEGYOLNYCSOQCPHLAGSPGIA 60
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db   352 SSFRAAYVNGFRMGILNGPYNSSCIPTKLSNMETLFDDEYINVRKYDPMYVEEGCA 411
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY   61 ASFHSAVSFLKANNPMPAST-SCCVPIARPRLDLLIDHNGNVYKTDVPDMVYEACGCS 119

```

Search completed: Thu Aug 17 10:16:42 2000
Job time : 39 secs.

CC LENGTH: 119 amino acids
CC TYPE: amino acids
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC HYPOHETICAL: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: Internal
CC ORIGINAL SOURCE:
SQ SEQUENCE 119 AA; 13161 MW; 75307 CN;

Query Match 100.0%; Score 916; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 4,26e-104;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 RARRPTCEPATPLCCRRDHYVDFQELGWRDWILOPEGYOLNYCGGCPHLAGSPGIA 60
QY 1 RARRPTCEPATPLCCRRDHYVDFQELGWRDWILOPEGYOLNYCGGCPHLAGSPGIA 60
61 ASFSHSAVSLKANNPWPASTSCCVPTARRPLSLTYLDHNGNVKTDVDMVVEACGCS 119
61 ASFSHSAVSLKANNPWPASTSCCVPTARRPLSLTYLDHNGNVKTDVDMVVEACGCS 119

RESULT 2
ID US-09-184-933-12 STANDARD; PRT: 119 AA.
AC xxxxxx
DE Sequence 12, Application US/09184933

CC GENERAL INFORMATION:
CC APPLICANT: Lee, Se-Jin
CC APPLICANT: Esquelea, Aurora F.
CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson, P.C.
CC STREET: 4225 Executive Square, Suite 1400
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: US
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC OPERATING SYSTEM: IBM compatible
CC SOFTWARE: FASTSEQ for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/09/184,933
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/274,215
CC FILING DATE: 13-JUL-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Halle, Ph.D., Lisa A.
CC REGISTRATION NUMBER: 38,347
CC REFERENCE/DOCKET NUMBER: 07265/040001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-678-5070
CC TELEFAX: 619-68-5099
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 119 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: Internal
SQ SEQUENCE 119 AA; 13161 MW; 75307 CN;

Query Match 100.0%; Score 916; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 4,26e-104;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 RARRPTCEPATPLCCRRDHYVDFQELGWRDWILOPEGYOLNYCGGCPHLAGSPGIA 60
QY 1 RARRPTCEPATPLCCRRDHYVDFQELGWRDWILOPEGYOLNYCGGCPHLAGSPGIA 60
61 ASFSHSAVSLKANNPWPASTSCCVPTARRPLSLTYLDHNGNVKTDVDMVVEACGCS 119
61 ASFSHSAVSLKANNPWPASTSCCVPTARRPLSLTYLDHNGNVKTDVDMVVEACGCS 119

RESULT 3
ID US-08-274-215-12 STANDARD; PRT: 119 AA.
AC xxxxxx
DE Sequence 12, Application US/08274215

CC GENERAL INFORMATION:
CC APPLICANT: Lee, Se-Jin
CC APPLICANT: Esquelea, Aurora F.
CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson P.C.
CC STREET: 4225 Executive Square, Suite 1400
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/274,215
CC FILING DATE: 13-JUL-1994
CC CLASSIFICATION: 536
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Halle, Lisa A.
CC REGISTRATION NUMBER: 38,347
CC REFERENCE/DOCKET NUMBER: 07265/040001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 212/765-5070
CC TELEFAX: 212/765-5070
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 119 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: both
CC MOLECULE TYPE: protein
SQ SEQUENCE 119 AA; 13161 MW; 75307 CN;

Query Match 100.0%; Score 916; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 4,26e-104;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 RARRPTCEPATPLCCRRDHYVDFQELGWRDWILOPEGYOLNYCGGCPHLAGSPGIA 60
QY 1 RARRPTCEPATPLCCRRDHYVDFQELGWRDWILOPEGYOLNYCGGCPHLAGSPGIA 60
61 ASFSHSAVSLKANNPWPASTSCCVPTARRPLSLTYLDHNGNVKTDVDMVVEACGCS 119
61 ASFSHSAVSLKANNPWPASTSCCVPTARRPLSLTYLDHNGNVKTDVDMVVEACGCS 119

RESULT 4
ID US-60-186-656-992 STANDARD: PRT: 131 AA.
AC xxxxxx
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DE Sequence 992, Application US/60186656
CC Sequence 992, Application US/60186656
CC GENERAL INFORMATION:
CC APPLICANT: Bonazzi, Vivien
CC TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
CC TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
CC FILE REFERENCE: CL000320
CC CURRENT APPLICATION NUMBER: US/60/186,656
CC CURRENT FILING DATE: 2000-03-03
CC NUMBER OF SEQ ID NOS: 1518
CC SOFTWARE: FastSeq for Windows Version 4.0
CC SEQ ID NO 992
CC LENGTH: 131
CC TYPE: PRT
CC ORGANISM: HUMAN
SQ SEQUENCE 131 AA: 14330 MW: 90159 CN;

Query Match 100.0%; Score 916; DB 3; Length 131;
Best Local Similarity 100.0%; Pred. No. 4,26e-104;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 RARRPTCEPATPLCCRDHYVDFOLGWRDWIIOPEGYOLNYCSGCCPPLAGSPGIA 72
QY 1 RARRPTCEPATPLCCRDHYVDFOLGWRDWIIOPEGYOLNYCSGCCPPLAGSPGIA 60
QY 73 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 131
QY 61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 119

RESULT 5
ID US-60-185-361-608 STANDARD: PRT: 153 AA.
AC xxxxxx
XX
XX
DE Sequence 608, Application US/60185361
CC Sequence 608, Application US/60185361
CC GENERAL INFORMATION:
CC APPLICANT: Bonazzi, Vivien
CC TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
CC TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
CC FILE REFERENCE: CL000291
CC CURRENT APPLICATION NUMBER: US/60/185,361
CC CURRENT FILING DATE: 2000-02-28
CC NUMBER OF SEQ ID NOS: 968
CC SOFTWARE: FastSeq for Windows Version 4.0
CC SEQ ID NO 608
CC LENGTH: 153
CC TYPE: PRT
CC ORGANISM: HUMAN
SQ SEQUENCE 153 AA: 16813 MW: 120970 CN;

Query Match 100.0%; Score 916; DB 3; Length 153;
Best Local Similarity 100.0%; Pred. No. 4,26e-104;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 35 RARRPTCEPATPLCCRDHYVDFOLGWRDWIIOPEGYOLNYCSGCCPPLAGSPGIA 94
QY 1 RARRPTCEPATPLCCRDHYVDFOLGWRDWIIOPEGYOLNYCSGCCPPLAGSPGIA 60

Db 95 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 153
QY 61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 119

RESULT 6
ID US-60-212-356-257 STANDARD: PRT: 274 AA.
AC xxxxxx
XX
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DE Sequence 257, Application US/60212356
CC Sequence 257, Application US/60212356
CC GENERAL INFORMATION:
CC APPLICANT: Beasley, Ellen
CC TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
CC TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
CC FILE REFERENCE: CL000677
CC CURRENT APPLICATION NUMBER: US/60/212,356
CC CURRENT FILING DATE: 2000-06-19
CC NUMBER OF SEQ ID NOS: 411
CC SOFTWARE: FastSeq for Windows Version 4.0
CC SEQ ID NO 257
CC LENGTH: 274
CC TYPE: PRT
CC ORGANISM: HUMAN
SQ SEQUENCE 274 AA: 29976 MW: 369765 CN;

Query Match 100.0%; Score 916; DB 23; Length 274;
Best Local Similarity 100.0%; Pred. No. 4,26e-104;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 156 RARRPTCEPATPLCCRDHYVDFOLGWRDWIIOPEGYOLNYCSGCCPPLAGSPGIA 215
QY 1 RARRPTCEPATPLCCRDHYVDFOLGWRDWIIOPEGYOLNYCSGCCPPLAGSPGIA 60
QY 216 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 274
QY 61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLIDHNGNVKTDVDMVVEACGCS 119

RESULT 7
ID US-09-521-978-4 STANDARD: PRT: 350 AA.
AC xxxxxx
XX
XX
DE Sequence 4, Application US/09521978
CC Sequence 4, Application US/09521978
CC GENERAL INFORMATION:
CC APPLICANT: Ford, John E.
CC APPLICANT: Mize, Nancy K.
CC APPLICANT: Dickson, Mark C.
CC APPLICANT: Atterburn, Matthew C.
CC TITLE OF INVENTION: Methods And Materials Relating To Novel
CC TITLE OF INVENTION: Activin/Inhibin-Like Polypeptides
CC FILE REFERENCE: HYS-2
CC CURRENT APPLICATION NUMBER: US/09/521,978
CC CURRENT FILING DATE: 2000-03-09
CC NUMBER OF SEQ ID NOS: 4
CC SOFTWARE: PatentIn Ver. 2.1
CC SEQ ID NO 4
CC LENGTH: 350
CC TYPE: PRT
CC ORGANISM: Homo sapiens
SQ SEQUENCE 350 AA: 38561 MW: 616706 CN;

Thu Aug 17 10:22:12 2000

US-08-765-662-12.rap

Page 7

OY 119 S 119

Search completed: Thu Aug 17 10:23:58 2000
Job time : 191 secs.

CC FRAGMENT TYPE: internal
CC ORIGINAL SOURCE:
SQ SEQUENCE 119 AA: 13161 MW: 75307 CN:
Query Match 100.0%; Score 916; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 2,84e-81;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 RARRRTPCEPATPLCCRRDHYVDFQELGWRDMLIQPEGYOLNYCSGCCPPHLASPGIA 60
1 RARRRTPCEPATPLCCRRDHYVDFQELGWRDMLIQPEGYOLNYCSGCCPPHLASPGIA 60
QY 1 RARRRTPCEPATPLCCRRDHYVDFQELGWRDMLIQPEGYOLNYCSGCCPPHLASPGIA 60
61 ASHSAVFSLLKANNPWPASTSCVPTARRPISLYLDHNGNVKTDVDMVVEACGCS 119
QY 61 ASHSAVFSLLKANNPWPASTSCVPTARRPISLYLDHNGNVKTDVDMVVEACGCS 119
RESULT 2
ID US-08-765-662-12 STANDARD: PRT: 119 AA.
XX xxxxxx
AC
DE Sequence 12, Application US/08765662
XX Sequence 12, Application US/08765662
CC Patent No. 5929213
CC GENERAL INFORMATION:
CC APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
CC NUMBER OF SEQUENCES: 14
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson
CC STREET: 4225 Executive Square, Suite 1400
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FastSeq Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/765.662
CC FILING DATE: 28-APR-1997
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08745
CC FILING DATE: 12-JUL-1995
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Halle, Ph.D., Lisa A.
CC REGISTRATION NUMBER: 38,347
CC REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3830)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-678-5070
CC TELEFAX: 619-678-5099
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 119 amino acids
CC TYPE: amino acids
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: internal
CC ORIGINAL SOURCE:
SQ SEQUENCE 119 AA: 13161 MW: 75307 CN:
Query Match 100.0%; Score 916; DB 2; Length 119;

Best Local Similarity 100.0%; Pred. No. 2,84e-81;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 RARRRTPCEPATPLCCRRDHYVDFQELGWRDMLIQPEGYOLNYCSGCCPPHLASPGIA 60
1 RARRRTPCEPATPLCCRRDHYVDFQELGWRDMLIQPEGYOLNYCSGCCPPHLASPGIA 60
QY 1 RARRRTPCEPATPLCCRRDHYVDFQELGWRDMLIQPEGYOLNYCSGCCPPHLASPGIA 60
61 ASHSAVFSLLKANNPWPASTSCVPTARRPISLYLDHNGNVKTDVDMVVEACGCS 119
QY 61 ASHSAVFSLLKANNPWPASTSCVPTARRPISLYLDHNGNVKTDVDMVVEACGCS 119
RESULT 3
ID US-08-274-215A-12 STANDARD: PRT: 119 AA.
XX xxxxxx
AC
DE Sequence 12, Application US/08274215A
XX Sequence 12, Application US/08274215A
CC Patent No. 5831054
CC GENERAL INFORMATION:
CC APPLICANT: Lee, Se-Jin
CC APPLICANT: Esqueja, Aurora F.
CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson, P.C.
CC STREET: 4225 Executive Square, Suite 1400
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: US
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: Windows95
CC SOFTWARE: FastSeq for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/274.215A
CC FILING DATE: 13-JUL-1994
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Halle, Ph.D., Lisa A.
CC REGISTRATION NUMBER: 38,347
CC REFERENCE/DOCKET NUMBER: 07265/040001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-678-5070
CC TELEFAX: 619-66-5099
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 119 amino acids
CC TYPE: amino acid
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: internal
SQ SEQUENCE 119 AA: 13161 MW: 75307 CN:
Query Match 100.0%; Score 916; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 2,84e-81;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 RARRRTPCEPATPLCCRRDHYVDFQELGWRDMLIQPEGYOLNYCSGCCPPHLASPGIA 60
1 RARRRTPCEPATPLCCRRDHYVDFQELGWRDMLIQPEGYOLNYCSGCCPPHLASPGIA 60
QY 1 RARRRTPCEPATPLCCRRDHYVDFQELGWRDMLIQPEGYOLNYCSGCCPPHLASPGIA 60
61 ASHSAVFSLLKANNPWPASTSCVPTARRPISLYLDHNGNVKTDVDMVVEACGCS 119
QY 61 ASHSAVFSLLKANNPWPASTSCVPTARRPISLYLDHNGNVKTDVDMVVEACGCS 119

OY 61 ASFSHSAVSLKANNPMPASTSCVPTARRPLSLYLIDHNGNVKTDVPMVEACGCS 119

RESULT 4
ID PCT-US95-08745-14 STANDARD: PRT: 350 AA.
XX xxxxxx

Sequence 14, Application PC/TUS9508745
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
City: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08745
FILING DATE: 12-JUL-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3830)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
TELEX:

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:

SEQUENCE 350 AA: 38561 MW: 616706 CN:

Query Match 100.0%; Score 916; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 2,84e-81;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 233 RARRPTCEPATPLCCRDHYVDQELGMDWILQPEGYOLNYCSGCPPLASPGIA 291
|||||
OY 1 RARRPTCEPATPLCCRDHYVDQELGMDWILQPEGYOLNYCSGCPPLASPGIA 60
|||||

DB 292 ASFSHSAVSLKANNPMPASTSCVPTARRPLSLYLIDHNGNVKTDVPMVEACGCS 350
|||||
OY 61 ASFSHSAVSLKANNPMPASTSCVPTARRPLSLYLIDHNGNVKTDVPMVEACGCS 119
|||||

RESULT 5
ID US-08-765-662-14 STANDARD: PRT: 350 AA.
XX xxxxxx

XX Sequence 14, Application US/08765662
DE
XX
CC Sequence 14, Application US/08765662
CC Patent No. 5929213
CC GENERAL INFORMATION:
CC APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
CC NUMBER OF SEQUENCES: 14
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson
CC STREET: 4225 Executive Square, Suite 1400
CC City: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,662
FILING DATE: 28-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08745
FILING DATE: 12-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3830)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
TELEX:

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:

SEQUENCE 350 AA: 38561 MW: 616706 CN:

Query Match 100.0%; Score 916; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 2,84e-81;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 232 RARRPTCEPATPLCCRDHYVDQELGMDWILQPEGYOLNYCSGCPPLASPGIA 291
|||||
OY 1 RARRPTCEPATPLCCRDHYVDQELGMDWILQPEGYOLNYCSGCPPLASPGIA 60
|||||

DB 292 ASFSHSAVSLKANNPMPASTSCVPTARRPLSLYLIDHNGNVKTDVPMVEACGCS 350
|||||
OY 61 ASFSHSAVSLKANNPMPASTSCVPTARRPLSLYLIDHNGNVKTDVPMVEACGCS 119
|||||

RESULT 6
ID US-08-482-577B-4 STANDARD: PRT: 352 AA.
XX xxxxxx

Sequence 4, Application US/08482577B
DE
XX
CC Sequence 4, Application US/08482577B
CC Patent No. 5807713

CC GENERAL INFORMATION:
CC APPLICANT: HOTTEN, GERTRUD
CC APPLICANT: NEIDHARDT, HELGE
CC APPLICANT: BECHTOLD, ROLF
CC APPLICANT: POHL, JENS
CC TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
CC TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
CC NUMBER OF SEQUENCES: 49
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: NIKAI, D. MARCELSTEIN, MURRAY, AND ORAM
CC STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
CC CITY: WASHINGTON
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/482,577B
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KLESNER, SHARON
CC REGISTRATION NUMBER: 36,335
CC REFERENCE/DOCKET NUMBER: P564-5010
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202/638-5000
CC TELEFAX: 202/638-4810
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 352 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC PUBLICATION INFORMATION:
CC DOCUMENT NUMBER: US 08/289,222
CC FILING DATE: 12-AUG-1994
CC SEQ SEQUENCE 352 AA: 39387 MW: 619423 CN:
CC
CC Query Match 68.7%; Score 629; DB 1; Length 352;
CC Best Local Similarity 62.8%; Pred. No. 6,57e-52;
CC Matches 76; Conservative 27; Mismatches 16; Indels 2; Gaps 2;
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CC Db 232 RVRRRGIDCGGSMCCROEFFVDFREIGWMDWITIOPEGYAMNFCGCPPLHAGMPGIS 291
CC 1 RARRRTCEPATPLCCRRDHVDFOLGWRDWITLOPEGYQLNYCGGCPPLHAGSPGIA 60
CC 292 ASFHITVNLITKANAAGTGTGSCCVPTSRRLSLIYDRSNITKTDIPMYVEAGCC 351
CC 61 ASHSAVSVFLKANNPW-PAS-TSCCVPTARRPLSLITLDHNGNVKTDVPMVVEAGCC 118
CC
CC Db 352 S 352
CC 119 S 119
CC
CC RESULT 7
CC ID US-08-455-550-11 STANDARD: PRT: 127 AA.
CC AC xxxxxx
CC DE Sequence 11, Application US/08455550
CC XX Sequence 11, Application US/08455550
CC CC Patent No. 5670338
CC GENERAL INFORMATION:
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CC APPLICANT: MURAKAMI, KAZUO
CC APPLICANT: UENO, NAOTO
CC APPLICANT: KATO, YUKIO
CC TITLE OF INVENTION: XENOPUS LAEVIS BONE MORPHOGENETIC PROTEINS AND USE THE
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: DIKE, Bronsteijn, Roberts & Cushman
CC STREET: 110 Water Street
CC CITY: Boston
CC STATE: MA
CC COUNTRY: USA
CC ZIP: 02109
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/455,550
CC FILING DATE: 31-MAY-1995
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/056,564
CC FILING DATE: 30-APR-1993
CC APPLICATION NUMBER: 07/577,892
CC FILING DATE: 05-SEP-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Eisenstein, Ronald I
CC REGISTRATION NUMBER: 30628
CC REFERENCE/DOCKET NUMBER: 40302-PWC-DIV
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 617-523-3400
CC TELEFAX: 617-523-6440
CC
CC INFORMATION FOR SEQ ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 127 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: N-terminal
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CC SEQ SEQUENCE 127 AA: 14256 MW: 78142 CN:
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CC Query Match 67.4%; Score 617; DB 1; Length 127;
CC Best Local Similarity 62.2%; Pred. No. 1.09e-50;
CC Matches 74; Conservative 24; Mismatches 21; Indels 0; Gaps 0;
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CC ID US-08-482-577B-2 STANDARD: PRT: 352 AA.
CC AC xxxxxx
CC DE Sequence 2, Application US/08482577B
CC XX Sequence 2, Application US/08482577B
CC CC Patent No. 5807713
CC GENERAL INFORMATION:
CC APPLICANT: HOTTEN, GERTRUD

Page 5

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CC STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
CC STREET: SUITE 330
CC CITY: WASHINGTON
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/482,5778
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KLESNER, SHARON
CC REGISTRATION NUMBER: 36,335
CC REFERENCE/DOCKET NUMBER: P564-5010
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202/638-5000
CC TELEFAX: 202/638-4810
CC INFORMATION FOR SEQ ID NO: 24:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 106 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
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XX Sequence 19, Application PC/TUS9400685
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XX Sequence 19, Application PC/TUS9400685
XX AC GENERAL INFORMATION:
XX AC APPLICANT: THE JOHNS HOPKINS UNIVERSITY
XX AC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
XX AC NUMBER OF SEQUENCES: 26
XX AC CORRESPONDENCE ADDRESS:
XX AC ADDRESSEE: Spensley Horn Jubas & Lubitz
XX AC STREET: 1680 Century Park East, Suite 500
XX AC CITY: Los Angeles
XX AC STATE: California
XX AC COUNTRY: US
XX AC ZIP: 90067
XX AC COMPUTER READABLE FORM:
XX AC MEDIUM TYPE: floppy disk
XX AC COMPUTER: IBM PC compatible
XX AC OPERATING SYSTEM: PC-DOS/MS-DOS
XX AC SOFTWARE: Patentn Release #1.0, Version #1.25
XX AC CURRENT APPLICATION DATA:
XX AC APPLICATION NUMBER: PCT/US94/00685
XX AC FILING DATE: 12-JAN-1994
XX AC

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CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (619) 455-5100  
CC TELEFAX: (619) 455-5110  
CC INFORMATION FOR SEQ ID NO: 21:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 121 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC IMMEDIATE SOURCE:  
CC CLONE: Inhibin beta A  
CC FEATURE:  
CC NAME/KEY: Protein  
CC LOCATION: 1..121  
CC  
SO SEQUENCE 121 AA; 13757 MW; 76294 CN;  
  
Query Match 54.4%; Score 498; DB 4; Length 121;  
Best Local Similarity 45.5%; Pred. No. 1,16e-38;  
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2.  
  
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QY 119 S 119  
  
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CC Patent No. 5808007  
CC GENERAL INFORMATION:  
CC APPLICANT: JOHNS HOPKINS UNIVERSITY  
CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3  
CC NUMBER OF SEQUENCES: 29  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: SPENSLER HORN JUBAS & LUBITZ  
CC STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR  
CC CITY: LOS ANGELES  
CC STATE: CALIFORNIA  
CC COUNTRY: US  
CC ZIP: 90067  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/481,377  
CC FILING DATE:  
CC CLASSIFICATION: 514  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US94/00666  
CC FILING DATE: 12-JAN-1994  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: WETHERELL, JR. PH.D., JOHN R.  
CC REGISTRATION NUMBER: 31,678  
CC REFERENCE/DOCKET NUMBER: FD2279 PCT  
CC TELECOMMUNICATION INFORMATION:
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CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 21:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 121 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC IMMEDIATE SOURCE:
 CC CLONE: Inhibin beta A
 CC FEATURE:
 CC NAME/KEY: Protein
 CC LOCATION: 1..121
 CC SEQUENCE 121 AA; 13757 MW; 76294 CN;

Query Match 54.4%; Score 498; DB 1; Length 121;
 Best Local Similarity 45.5%; Pred. No. 1,16e-38;
 Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;

Db 1 RRRRGLECDGKVNICKKQFVSEFKDIGNMDWIAPSGYHANYCEGECPSHIAGTSGSS 60
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 DE Sequence 19, Application US/08491835
 CC Sequence 19, Application US/08491835
 CC Patent No. 5821056
 CC GENERAL INFORMATION:
 CC APPLICANT: THE JOHNS HOPKINS UNIVERSITY
 CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
 CC NUMBER OF SEQUENCES: 26
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Jubas & Lubitz
 CC STREET: 1880 Century Park East, Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentin Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/491,835
 CC FILING DATE: 23-OCT-1995
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US94/00685
 CC FILING DATE: 12-JAN-1994
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Wetherell, Jr. Ph.D., John R.
 CC REGISTRATION NUMBER: 31,678
 CC REFERENCE/DOCKET NUMBER: FD3288
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100

CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 19:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 121 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC IMMEDIATE SOURCE:
 CC CLONE: Inhibin betaA
 CC FEATURE:
 CC NAME/KEY: Protein
 CC LOCATION: 1..121
 CC SEQUENCE 121 AA; 13757 MW; 76294 CN;

Query Match 54.4%; Score 498; DB 2; Length 121;
 Best Local Similarity 45.5%; Pred. No. 1,16e-38;
 Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;

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 CC Sequence 21, Application US/09153733A
 CC Patent No. 6025475
 CC GENERAL INFORMATION:
 CC APPLICANT: JOHNS HOPKINS UNIVERSITY
 CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
 CC NUMBER OF SEQUENCES: 29
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
 CC STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
 CC CITY: LOS ANGELES
 CC STATE: CALIFORNIA
 CC COUNTRY: US
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentin Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/09/153,733A
 CC FILING DATE:
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: 08/481,377
 CC FILING DATE:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: WETHERELL, JR. Ph.D., JOHN R.
 CC REGISTRATION NUMBER: 31,678
 CC REFERENCE/DOCKET NUMBER: FD2279 PCT
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110

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CC INFORMATION FOR SEQ ID NO: 21:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 121 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC IMMEDIATE SOURCE:  
CC CLONE: Inhibin beta A  
CC FEATURE:  
CC NAME/KEY: Protein  
CC LOCATION: 1..121  
SQ SEQUENCE 121 AA; 13757 MW; 76294 CN;  
  
Query Match 54.4%; Score 498; DB 3; Length 121;  
Best Local Similarity 45.5%; Pred No. 1,16e-38;  
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2.  
  
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DE Sequence 23, Application US/08455559  
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CC Patent No. 5801014  
CC GENERAL INFORMATION:  
CC APPLICANT: LEE, SE-JIN  
CC APPLICANT: HUYNH, THANH  
CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5  
CC NUMBER OF SEQUENCES: 27  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: SPENLEY HORN JUBAS & LOBITZ  
CC STREET: 1860 CENTURY PARK EAST, FIFTH FLOOR  
CC CITY: LOS ANGELES  
CC STATE: CALIFORNIA  
CC COUNTRY: US  
CC ZIP: 90067  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/455,559  
CC FILING DATE: 31-MAY-1995  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/003,144  
CC FILING DATE: 12-JAN-1993  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: WETHERELL, JR. PH.D., JOHN R.  
CC REGISTRATION NUMBER: 31,678  
CC REFERENCE/DOCKET NUMBER: PD2280  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 619/455-5100  
CC TELEFAX: 619-455-5110  
CC
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CC INFORMATION FOR SEQ ID NO: 23:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 122 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC IMMEDIATE SOURCE:
CC CLONE: Inhibin-beta-alpha
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CC NAME/KEY: Protein
CC LOCATION: 1..122
CC SEQUENCE 122 AA; 13894 MW; 77513 CN;

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Best local similarity 45.5%; Pred. No. 1,16e-36;
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2.

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CC SEQUENCE CHARACTERISTICS:  
CC     LENGTH: 121 amino acids  
CC     TYPE: amino acid  
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CC     TOPOLOGY: linear  
CC     MOLECULE TYPE: protein  
CC     IMMEDIATE SOURCE:  
CC     CLONE: Inhibin beta A  
CC     FEATURE:  
CC NAME/KEY: Protein  
CC LOCATION: 1..121  
SQ SEQUENCE 121 AA; 13757 MW; 76294 CN;  
  
Query Match          54.4%; Score 498; DB 3; Length 121;  
Best Local Similarity 45.5%; Pred No. 1,16e-38;  
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CC GENERAL INFORMATION:  
CC APPLICANT: LEE, SE-JIN  
CC APPLICANT: HOYNH, THANH  
CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5  
CC NUMBER OF SEQUENCES: 27  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: SPENLEY HORN JUBAS & LOBITZ  
CC STREET: 1860 CENTURY PARK EAST, FIFTH FLOOR  
CC CITY: LOS ANGELES  
CC STATE: CALIFORNIA  
CC COUNTRY: US  
CC ZIP: 90067  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/455,559  
CC FILING DATE: 31-MAY-1995  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/003,144  
CC FILING DATE: 12-JAN-1993  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: WETHERELL, JR. PH.D., JOHN R.  
CC REGISTRATION NUMBER: 31,678  
CC REFERENCE/DOCKET NUMBER: PD2280  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 619/455-5100  
CC TELEFAX: 619-455-5110  
CC
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(TM)

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Gap 11

85661 seqs, 30989116 residues

Listing first 45

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Mean 40.432; Variance 56.147; scale 0.720

ived by analysis of the total score distribution.

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U00002	350	INHE_RAT	INHIBIN BETA E CHAIN P	1.53e-22
U00003	352	INHC_MOUSE	INHIBIN BETA C CHAIN P	2.42e-14
U00004	352	INHE_HUMAN	INHIBIN BETA C CHAIN P	1.2e-14
U00005	426	INHA_HORSE	INHIBIN BETA A CHAIN P	1.22e-11
U00006	426	INHA_SHEEP	INHIBIN BETA A CHAIN P	9.00e-11
U00007	424	INHA_MOUSE	INHIBIN BETA A CHAIN P	2.48e-10
U00008	424	INHA_RAT	INHIBIN BETA A CHAIN P	2.49e-10
U00009	424	INHA_PIG	INHIBIN BETA A CHAIN P	2.49e-10
U00010	426	INHA_HUMAN	INHIBIN BETA A CHAIN P	2.49e-10
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U00012	424	INHA_CHICK	INHIBIN BETA A CHAIN P	2.75e-10
U00013	391	INHB_CHICK	INHIBIN BETA B CHAIN P	2.00e-10
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U00016	407	INHB_BOVIN	INHIBIN BETA B CHAIN P	1.03e-10
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U00020	398	BMPA_XENLA	BONE MORPHOGENETIC PRO	1.00e-68
U00021	398	BMPA_XENLA	BONE MORPHOGENETIC PRO	1.00e-68
U00022	401	BMPA_XENLA	BONE MORPHOGENETIC PRO	6.84e-68
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24	352	BMP4, RAD	BONE MORPHOGENETIC PRO	6.84e-68
25	352	BMP4, RAD	BONE MORPHOGENETIC PRO	6.84e-68
26	351	BMP4, CHICK	BONE MORPHOGENETIC PRO	1.30e-67
27	350	BMP2, RAT	BONE MORPHOGENETIC PRO	2.46e-67
28	350	BMP2, MOUSE	BONE MORPHOGENETIC PRO	2.46e-67
29	350	BMP2, RAJIT	BONE MORPHOGENETIC PRO	2.46e-67
30	350	BMP2, HUJAN	BONE MORPHOGENETIC PRO	2.46e-67
31	350	BMP2, DADAA	BONE MORPHOGENETIC PRO	2.46e-67
32	350	BMP4, RAJIT	BONE MORPHOGENETIC PRO	2.46e-67
33	346	BMP2, CHICK	BONE MORPHOGENETIC PRO	3.18e-65
34	341	GDF1, HUJAN	EMBRYONIC GROWTH/DIFFE	7.75e-65
35	340	UNIV, STEPU	UNIVIN PRECURSOR.	1.47e-64
36	331	DVR1, XEMLA	DVR-1 PROTEIN PRECURSOR	4.52e-62
37	331	BMP6, HUJAN	BONE MORPHOGENETIC PRO	4.52e-62
38	327	BMP6, RAD	BONE MORPHOGENETIC PRO	5.73e-61
39	327	BMP6, MOUSE	BONE MORPHOGENETIC PRO	5.73e-61
40	326	DECA, DROPS	DECAEPNTALPELIC PROTEI	1.08e-61
41	324	DECA, DROST	DECAEPNTALPELIC PROTEI	3.84e-60
42	324	DECA, DROST	DECAEPNTALPELIC PROTEI	3.84e-60
43	323	DECA, DROME	DECAEPNTALPELIC PROTEI	7.24e-60
44	321	BMP7, MOUSE	BONE MORPHOGENETIC PRO	2.53e-60
45	320	BMP7, HUJAN	BONE MORPHOGENETIC PRO	4.85e-59

ALIGNMENTS

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1
INBE.MOUSE STANDARD; PRT; 350 AA.
008717;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INHIBIN BETA E CHAIN PRECURSOR (ACTIVIN BETA-E CHAIN).
INBE.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
SEQUENCE FROM N.A.
TISSUE=LIVER;
MEDLINE; 97096313.
Fang J., Yin W., Smiley E., Wang S.Q., Bonadio J.:
"Molecular cloning of the mouse activin beta E subunit gene."
Biochem. Biophys. Res. Commun. 228:669-674(1996).
[2]
MAPING.
MEDLINE; 97224404.
Fang J., Wang S.Q., Smiley E., Bonadio J.:
"Genes coding for mouse activin beta C and beta E are closely linked
and exhibit a liver-specific expression pattern in adult tissues."
Biochem. Biophys. Res. Commun. 231:655-661(1997).
-1- FUNCTION: INHIBINS ARE GONADAL GLYCOPROTEIDS THAT INHIBIT THE
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
ACTIVINS ACTIVATE THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE
GROWTH AND DIFFERENTIATION OF EMBRYONAL CARCINOMA CELLS, INDUCE
ERYTHROPOIESIS, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL
CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL
DEVELOPMENT.
-1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
-----
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EMBL; D96386; AB53801.1; -
MGD; MGI:109269; INBE.
PRAW; P00019; TGF-beta; 1.
PRINTS; P000438; GFCYSKNOT.

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KW PROSITE PS00250; TGF-BETA-1; 1.
FM Follicleotropin inhibitor; Contracptive; Hormone; Glycoprotein; signal.
FT SIGNAL 1 21
FT PROPEP 22 236
FT CHAIN 237 350
FT DISULFID 240 248
FT DISULFID 247 315
FT DISULFID 276 347
FT DISULFID 280 349
FT DISULFID 314 314
FT CARBOHYD 198 198
SQ SEQUENCE 350 AA; 39057 MW; F37C76C8061DBAD9 CRC64;

Query Match 98.9%; Score 906; DB 1; Length 350;
Best Local Similarity 97.5%; Pred. No. 1,236-229;
Matches 116; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 232 RARRRTPCEPPPEPLPCRRDHYDVEPEGLRWMLIQPEGYOLNCSGCPPLHAGSP31A 291
|||||
1 RARRRTPCEPPAPPLPCRRDHYDVEPEGLRWMLIQPEGYOLNCSGCPPLHAGSP31A 60

Oy 292 ASFSHSAVFSLTKANNWPAGSSCCVPTARRPSTLXLDHNNVYKTPVPMVYEAAGCS 350
|||||
61 ASFSHSAVFSLTKANNWPAGSSCCVPTARRPSTLXLDHNNVYKTPVPMVYEAAGCS 119

RESULT 2 STANDARD; PRT: 350 AA.
ID IIBE RAT
AC 088959;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INHIBIN BETA E CHAIN PRECURSOR (ACTIVIN BETA-E CHAIN).
GN INBE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER, AND LUNG;
RA O'Bryan M.K., Sebire K., Hedger M.P., Hearn M.T.W., de Kretser D.M.;
RT "The cloning and regulation of the rat activin subunit."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: INHIBINS ARE GONADAL GLYCOPETIDES THAT INHIBIT THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVINS ACTIVATE THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE
CC GROWTH AND DIFFERENTIATION OF EMBRYONAL CARCINOMA CELLS. INDUCE
CC ERYTHROPOIESIS. STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL
CC CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL
CC DEVELOPMENT.
CC -I- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS (BY
CC SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: AF089825; AAC36741.1; -
DR PFM, PF00019; TGF-beta.1.
DR PRINTS: PR00436; GFCYSKNOT.
DR PROSITE: PS00250; TGF-BETA-1; 1.
FM Follicleotropin inhibitor; Contracptive; Hormone; Glycoprotein; signal.
FT SIGNAL 1 21
FT PROPEP 22 236
FT CHAIN 237 350
FT DISULFID 240 248
FT DISULFID 247 315
FT DISULFID 276 347
FT DISULFID 314 314
FT CARBOHYD 198 198
SQ SEQUENCE 350 AA; 39057 MW; F37C76C8061DBAD9 CRC64;

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[illegible]

DR EMBL: U40773: AAC52723.1: -
 DR EMBL: U40772: AAC52723.1: JOINED.
 DR EMBL: U95962: AAC53164.1: -
 DR HSSP: P18075: 1BMP
 DR MCD: MGI:105932: INHBC.
 DR PFAM: PF00019: TGF-beta: 1.
 DR PRINTS: PR00438: GFCYSKNOT.
 DR PRINTS: PR00672: INHIBINBC.
 DR PROSITE: PS00250: TGF_BETA_1: 1.
 DR FOLLITROPIN inhibitor: Contraceptive: Hormone: Glycoprotein: Signal.
 KW FOLLITROPIN inhibitor: Contraceptive: Hormone: Glycoprotein: Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 236
 FT CHAIN 237 352
 FT DISULFID 240 248
 FT DISULFID 247 317
 FT DISULFID 276 349
 FT DISULFID 280 351
 FT DISULFID 316 316
 FT CARBOHYD 111 111
 FT CARBOHYD 143 143
 FT CARBOHYD 161 161
 FT CARBOHYD 173 173
 FT CONFLICT 243 243
 FT SEQUENCE 352 AA; 39401 MW; 220812FD73717185 CRC64;
 SQ
 Query Match 69.0%; Score 632; DB 1; Length 352;
 Best Local Similarity 63.6%; Pred. No. 2,46e-148;
 Matches 77; Conservative 26; Mismatches 16; Indels 2; Gaps 2;
 Db 232 RVRRRGIDCGGSRMCCQGFVDFREIGAMDWIIOPGYAMNCTGCPPLHVGMGIS 291
 QY 1 RARRPTPCBPATPLCCRRDHYVDFELGMRDWIOLPGYGLNCSGGCPHLGSGEIA 60
 Db 292 ASFHRAVNLKANAAGTGGSCCVPTARRPLSLIYYDRDSINVTIDIPDMVVEAGCS 351
 QY 61 ASFHRAVSLKANNPW-PAS-TSCVPTARRPLSLIYLDHNGNVKTDVDMVVEAGCG 118
 Db 352 S 352
 QY 119 S 119
 RESULT 4
 ID IHBH-HUMAN STANDARD; PRT; 352 AA.
 AC P55103;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 01-NOV-1997 (Rel. 35, Last annotation update)
 GN INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE: 95126961.
 RA Hoeft G., Neidhardt H., Schneider C., Pohl J.;
 RT "Cloning of a new member of the TGF-beta family: a putative new
 activin beta C chain."
 RL Biochem. Biophys. Res. Commun. 206:608-613(1995).
 CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPOLYMER THAT INHIBITS THE
 SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
 ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE
 GROWTH AND DIFFERENTIATION OF EMBRYONAL CARCINOMA CELLS, INDUCE
 ERYTHROPOIESIS, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL
 CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL
 DEVELOPMENT.
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL: X82540: CA57890.1: -
 DR HSSP: P18075: 1BMP.
 DR MIM: 601233: -
 DR PFAM: PF00019: TGF-beta: 1.
 DR PRINTS: PR00438: GFCYSKNOT.
 DR PRINTS: PR00672: INHIBINBC.
 DR PROSITE: PS00250: TGF_BETA_1: 1.
 DR FOLLITROPIN inhibitor: Contraceptive: Hormone: Glycoprotein: Signal.
 KW FOLLITROPIN inhibitor: Contraceptive: Hormone: Glycoprotein: Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 236
 FT CHAIN 237 352
 FT DISULFID 240 248
 FT DISULFID 247 317
 FT DISULFID 276 349
 FT DISULFID 280 351
 FT DISULFID 316 316
 FT CARBOHYD 110 110
 FT CARBOHYD 143 143
 FT CARBOHYD 161 161
 FT SEQUENCE 352 AA; 38238 MW; 496476AD82562D3E CRC64;
 SQ
 Query Match 67.2%; Score 616; DB 1; Length 352;
 Best Local Similarity 63.9%; Pred. No. 1,21e-143;
 Matches 76; Conservative 26; Mismatches 15; Indels 2; Gaps 2;
 Db 234 HRRGIDCGGSRMCCQGFVDFREIGAMDWIIOPGYAMNCTGCPPLHVGMGIS 293
 QY 3 RRRPTPCBPATPLCCRRDHYVDFELGMRDWIOLPGYGLNCSGGCPHLGSGEIA 62
 Db 294 FHTAVNLKANAAGTGGSCCVPTARRPLSLIYYDRDSINVTIDIPDMVVEAGCS 352
 QY 63 FHSRAVSLKANNPW-PAS-TSCVPTARRPLSLIYLDHNGNVKTDVDMVVEAGCG 119
 RESULT 5
 ID IHBH-HORSE STANDARD; PRT; 426 AA.
 AC P55102;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE 01-NOV-1997 (Rel. 35, Last annotation update)
 GN INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVARY;
 RX MEDLINE: 96031670.
 RA Yoshida S., Yamamoto K., Hasegawa T., Ikeda A., Suzuki M.,
 RA Chang K., Matsuyama S., Nishihara M., Takahashi M.;
 RT "Molecular cloning of cDNA for equine ovarian inhibin/activin beta A
 subunit."
 RL J. Vet. Med. Sci. 57:469-473(1995).
 CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPOLYMER THAT INHIBITS THE
 SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
 ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
 IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
 CC ACTIVIN A IS A DIMER OF BETA-A.
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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EMBL: D50326; BAA0862.1; -

HSSP: P18075; IBM.

PFAM: PF00019; TGF-beta; 1.

PRINTS: PR00438; GFCYSKNOT.

PROSITE: PS00250; TGF_BETA_1; 1.

Follicle-inhibitor: Contrapeptive; Hormone; Glycoprotein; Signal.

SIGNAL

PROPEP

CHAIN

DISULFID

DISULFID

DISULFID

DISULFID

DISULFID

CARBOHYD

SEQUENCE

426 AA; 47709 MW; E481060B8368A77D CRC64;

Query Match

Best Local Similarity 47.18; Score 506; DB 1; Length 426;

Matches 57; Conservative 30; Mismatches 32; Indels 2; Gaps 1;

DB 306 RRRRGLECDGKVNICKCKKQFVSEFKDIGMNDWIAPSGYHANYCEGCEPSHIATSGSS 365

1 RARRPTCEPATPLCCRDHYDFQELGMDWIIQPEGYQLYNCGCPHILASPGIA 60

366 LSFHSVINYQVLRGHNPPANLKSCCVPTKLRPMMLYYDDGQNIKKIDIONMIVEEGCC 425

61 ASFHSNVFL-L-KANMPASTSCCVPTARRPLSLIYLDHNGNVYKIDVPMVEACGC 118

DB 426 S 426

1

QY 119 S 119

RESULT 6

ID IHA_SHEEP STANDARD: PRT: 425 AA.

AC P43032;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DT INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).

INHBA.

Ovis aries (Sheep).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.

SEQUENCE FROM N.A.

Fleming J.S., Galloway S.M., Crawford R.J., Tisdall D.J.,

Greenwood P.J.,

"Tissue-specific variation in the length of the 5' untranslated region of the beta A-inhibin mRNA in sheep."

Mol. Reprod. Dev. 40:1-8(1995).

-1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.

-1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.

INHIBIN A IS A DIMER OF ALPHA AND BETA-A.

INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

ACTIVIN A IS A DIMER OF BETA-A.

ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.

-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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EMBL: L19218; AAC41621.1; -

HSSP: P18075; IBM.

PFAM: PF00019; TGF-beta; 1.

PRINTS: PR00438; GFCYSKNOT.

PROSITE: PS00250; TGF_BETA_1; 1.

Follicle-inhibitor: Contrapeptive; Hormone; Glycoprotein; Signal.

SIGNAL

PROPEP

CHAIN

DISULFID

DISULFID

DISULFID

DISULFID

CARBOHYD

SEQUENCE

425 AA; 47565 MW; C910F7F64FF82F67 CRC64;

Query Match

Best Local Similarity 46.38; Score 503; DB 1; Length 425;

Matches 56; Conservative 31; Mismatches 32; Indels 2; Gaps 2;

DB 305 RRRRGLECDGKVNICKCKKQFVSEFKDIGMNDWIAPSGYHANYCEGCEPSHIATSGSS 364

1 RARRPTCEPATPLCCRDHYDFQELGMDWIIQPEGYQLYNCGCPHILASPGIA 60

365 LSFHSVINYQVLRGHNPPANLKSCCVPTKLRPMMLYYDDGQNIKKIDIONMIVEEGCC 424

61 ASFHSNVFL-L-KANMPASTSCCVPTARRPLSLIYLDHNGNVYKIDVPMVEACGC 118

DB 425 S 425

1

QY 119 S 119

RESULT 7

ID IHA_MOUSE STANDARD: PRT: 424 AA.

AC Q04998;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DT INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).

INHBA.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

SEQUENCE FROM N.A.

Albano P.M., Groome N., Smith J.C.,

"Activins are expressed in preimplantation mouse embryos and in ES and EC cells and are regulated on their differentiation."

Development 117:711-723(1993).

-1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.

-1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.

INHIBIN A IS A DIMER OF ALPHA AND BETA-A.

INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

ACTIVIN A IS A DIMER OF BETA-A.

ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.

-1- TISSUE SPECIFICITY: UTERUS, OVARY, AND LIVER.

-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC -----
DR EMBL: X69619; CAA49325.1; -
DR PIR: S31440; S31440.
DR HSSP: P18075; 1BMP.
DR MGD: MGI:96570; INHBA.
DR PFAM: PF00688; TGF-beta; 1.
DR PFAM: PF00688; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR00670; INHIBINB.
DR PROSITE: PS00250; TGF_BETA_1; 1.
DR FOLLITROPIN inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 308
FT PROPEP 1 308
FT CHAIN 309 424 INHIBIN BETA A CHAIN.
FT DISULFID 312 320 BY SIMILARITY.
FT DISULFID 319 389 BY SIMILARITY.
FT DISULFID 348 421 BY SIMILARITY.
FT DISULFID 352 423 BY SIMILARITY.
FT DISULFID 388 388 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 165 165 POTENTIAL.
SQ SEQUENCE 424 AA; 47392 MW; 80C251B8754A7213 CRC64;

Query Match 54.4%; Score 498; DB 1; Length 424;
Best Local Similarity 45.5%; Pred. No. 2.49e-109;
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;

Db 304 RRRRGLECDGKVNICKKOFVSEFKDIGNMDWIIAPSGYHANYCEGPCSHIAGTSGSS 363
1 RARRPTPCPEPATPLCCRDHYVDFQELGRDWIILOPEGYQLNYCSGCCPPLAGSPGIA 60
Db 364 LSFHSTVINHYRMGHSFPANLKSVCVPTKLRPMSMLYDDGONIIRKDIQNMIVCEGC 423
61 ASFSHSAVES-L-LKANNPWPASTSCCVPTARRPLSLLYLDHNGNVKTDVPMVVEACGC 118
Db 424 S 424
QY 119 S 119
RESULT 8
ID INHBA_RAT STANDARD: PRT; 424 AA.
AC P18331:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
GN INHBA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 91042598.
RA Woodruff T.K., Meunier H., Jones P.B.C., Hsueh A.J.W., Mayo K.E.;
RT "Rat inhibin: molecular cloning of alpha- and beta-subunit
RT complementary deoxyribonucleic acids and expression in the ovary."
RL Mol. Endocrinol. 1:561-568(1987).
CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPOLYPEPTIDE THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF BETA-A.
CC ACTIVIN A IS A DIMER OF BETA-A.

CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M37482; AAA41436.1; -
DR PIR: B40056; B40056.
DR HSSP: P18075; 1BMP.
DR PFAM: PF00688; TGF-beta; 1.
DR PFAM: PF00688; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR00670; INHIBINB.
DR PROSITE: PS00250; TGF_BETA_1; 1.
DR FOLLITROPIN inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
KW FOLLITROPIN inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 308
FT PROPEP 1 308
FT CHAIN 309 424 INHIBIN BETA A CHAIN.
FT DISULFID 312 320 BY SIMILARITY.
FT DISULFID 319 389 BY SIMILARITY.
FT DISULFID 348 421 BY SIMILARITY.
FT DISULFID 352 423 BY SIMILARITY.
FT DISULFID 388 388 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 165 165 POTENTIAL.
SQ SEQUENCE 424 AA; 47406 MW; B2DAF7917FA50984 CRC64;

Query Match 54.4%; Score 498; DB 1; Length 424;
Best Local Similarity 45.5%; Pred. No. 2.49e-109;
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;

Db 304 RRRRGLECDGKVNICKKOFVSEFKDIGNMDWIIAPSGYHANYCEGPCSHIAGTSGSS 363
1 RARRPTPCPEPATPLCCRDHYVDFQELGRDWIILOPEGYQLNYCSGCCPPLAGSPGIA 60
Db 364 LSFHSTVINHYRMGHSFPANLKSVCVPTKLRPMSMLYDDGONIIRKDIQNMIVCEGC 423
61 ASFSHSAVES-L-LKANNPWPASTSCCVPTARRPLSLLYLDHNGNVKTDVPMVVEACGC 118
Db 424 S 424
QY 119 S 119
RESULT 9
ID INHBA_PIG STANDARD: PRT; 424 AA.
AC P03970:
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
GN INHBA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 86092207.
RA Mason A.U., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,
RA Guillemin R., Niall H., Seeburg P.H.;
RT "Complementary DNA sequences of ovarian follicular fluid inhibin show
RT precursor structure and homology with transforming growth
RL factor-beta." Nature 318:659-663(1985).
RL Nature 318:659-663(1985).
RN (2)
RN SEQUENCE OF 309-323.
RC TISSUE-FOLLICULAR FLUID;
RX MEDLINE: 92355604.

RA Nakamura T., Asashima M., Eto Y., Takio K., Uchiyama H., Moriya N.,
RA Aizumi T., Yashiro T., Sugino K., Titani K., Sugino H.;
RT "Isolation and characterization of native activin B.";
RT J. Biol. Chem. 267:16385-16389(1992).
CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC or send an email to license@isb-sib.ch).
DR EMBL: X03266; CA27020.1; -
DR PIR: A01393; WPGBA.
DR HSSP: P18075; IBM.
DR PFAM: PF00019; TGF-beta; 1.
DR PFAM: PF00688; TGF-propeptide; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR00670; INHIBINBA.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Follitropin inhibitor; Contrareptive; Hormone; glycoprotein; signal.
FT SIGNAL 1 308
FT PROPEP 1 308
FT CHAIN 1 308
FT DISULFID 309 424 INHIBIN BETA A CHAIN.
FT DISULFID 312 320 BY SIMILARITY.
FT DISULFID 319 389 BY SIMILARITY.
FT DISULFID 348 421 BY SIMILARITY.
FT DISULFID 352 423 BY SIMILARITY.
FT DISULFID 388 388 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 165 165 POTENTIAL.
SQ SEQUENCE 424 AA; 47476 MW; 436BC6226FDAF52 CRC64;
Query Match 54.4%; Score 498; DB 1; Length 424;
Best Local Similarity 45.5%; Pred. No. 2,49e-109;
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
Db 304 RRRRGLECDKVNICKKPFVSKFDIGWMDWITAPSGYHANYCEGPCPSHIATSGSS 363
1 RARRTPICEPATPLCCRDHYVDFELGWRDWILOPGYOLNCSGCGPHLAGSPGIA 60
364 LSFHSTVINHYRMGHSFANLKSCVPTKLRPSMSLYDDGQNIKKDIONMIVECGC 423
61 ASFSHSAVRS-L-LKANNWPASTSCVPTARRPLSLYLIDHNGNVKTDVDMVEACGC 118
Db 424 S 424
QY 119 S 119
RESULT 10
ID INBA_BOVIN STANDARD. PRT: 425 AA.
AC P07995;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
GN INBA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE: 95112839.
RA Thompson D.A., Cronin C.N., Martin F.;
RT "Genomic cloning and sequence analyses of the bovine alpha-, beta A-
RT and beta B-inhibin/activin genes. Identification of transcription
RT factor AP-2-binding sites in the 5'-flanking regions by DNase I
RT footprinting.";
RL Eur. J. Biochem. 226:751-764(1994).
RN [2]
RP SEQUENCE OF 258-425 FROM N.A.
RC TISSUE=FOLLICULAR FLUID;
RX MEDLINE: 86205842.
RA Forage R.G., Ring J.M., Brown R.W., McInerney B.V., Cobon G.S.,
RA Gregson R.P., Robertson D.M., Morgan F.J., Hearn M.T.W., Findlay J.K.,
RA Wettenhall R.E.H., Burger H.G., de Kretser D.M.;
RT "Cloning and sequence analysis of cDNA species coding for the two
RT subunits of inhibin from bovine follicular fluid.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3091-3095(1986).
CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC or send an email to license@isb-sib.ch).
DR EMBL: U16239; AAB60627.1; -
DR EMBL: U16238; AAB60627.1; JOINED.
DR EMBL: M13274; AAA97415.1; -
DR PIR: B25732; B25732.
DR HSSP: P18075; IBM.
DR PFAM: PF00019; TGF-beta; 1.
DR PFAM: PF00688; TGF-propeptide; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR00670; INHIBINBA.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Follitropin inhibitor; Contrareptive; Hormone; glycoprotein;
KW signal.
FT SIGNAL 1 28
FT PROPEP 1 28
FT CHAIN 1 28
FT DISULFID 29 309 BY SIMILARITY.
FT DISULFID 310 425 INHIBIN BETA A CHAIN.
FT DISULFID 313 321 BY SIMILARITY.
FT DISULFID 320 390 BY SIMILARITY.
FT DISULFID 349 422 BY SIMILARITY.
FT DISULFID 353 424 BY SIMILARITY.
FT DISULFID 389 389 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 165 165 POTENTIAL.
SQ SEQUENCE 425 AA; 47521 MW; 2D8799D7197CDA37 CRC64;
Query Match 54.4%; Score 498; DB 1; Length 425;
Best Local Similarity 45.5%; Pred. No. 2,49e-109;
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
Db 305 RRRRGLECDKVNICKKPFVSKFDIGWMDWITAPSGYHANYCEGPCPSHIATSGSS 364
1 RARRTPICEPATPLCCRDHYVDFELGWRDWILOPGYOLNCSGCGPHLAGSPGIA 60
365 LSFHSTVINHYRMGHSFANLKSCVPTKLRPSMSLYDDGQNIKKDIONMIVECGC 424
61 ASFSHSAVRS-L-LKANNWPASTSCVPTARRPLSLYLIDHNGNVKTDVDMVEACGC 118
QY 61 ASFSHSAVRS-L-LKANNWPASTSCVPTARRPLSLYLIDHNGNVKTDVDMVEACGC 118

Db 425 S 425
OY 119 S 119

RESULT 11
ID ITHBA_HUMAN STANDARD: PRT: 426 AA.
AC P08476; Q14599.
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN) (ERYTHROID DIFFERENTIATION PROTEIN) (EDF).
GN INHBA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
[1]
SEQUENCE FROM N.A.
RA MEDLINE: 86186863.
RA Mason A.J., Miall H.D., Seeburg P.H.;
RT "Structure of two human ovarian inhibins.";
RL Biochem. Biophys. Res. Commun. 135:957-964(1986).
[2]
SEQUENCE FROM N.A.
RA MEDLINE: 88190086.
RA Murata M., Eto Y., Shibai H., Sakai M., Muramatsu M.;
RT "Erythroid differentiation factor is encoded by the same mRNA as that of the inhibin beta A chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2434-2438(1988).
[3]
SEQUENCE FROM N.A.
RA MEDLINE: 92135888.
RA Tanimoto K., Handa S.I., Ueno N., Murekami K., Fukumizu A.;
RT "Structure and sequence analysis of the human activin beta A subunit gene.";
RL DNA Seq. 2:103-110(1991).
[4]
SEQUENCE OF 311-426 FROM N.A.
RX MEDLINE: 87005283.
RX Stewart A.G., Milborrow H.M., Ring J.M., Crowther C.E., Forage R.G.;
RL "Human inhibin genes. Genomic characterisation and sequencing.";
RL FEBS Lett. 206:329-334(1986).
[5]
SEQUENCE OF 311-426 FROM N.A.
RP TISSUE-TESTIS:
RP Berg H., Walter M., Northern M.;
RT Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: M13436; AAA59166.1; -;
DR EMBL: X04447; CAA28041.1; -;
DR EMBL: X57578; CAA40805.1; -;
DR EMBL: X57579; CAA40805.1; JOINED.
DR EMBL: X57579; CAA40806.1; -;
DR EMBL: J03634; AAA35787.1; -;

DR EMBL: A14422; CAA01159.1; -;
DR EMBL: X72498; CAA51163.1; -;
DR PIR: A30884; A30884.
DR PIR: B24248; B24248.
DR PIR: B23556; B23556.
DR PIR: S30488; S30488.
DR HSSP: P18075; IBMP.
DR MIM: 147290; -;
DR PFAM: PF00019; TGF-beta; 1.
DR PFAM: PF00688; TGF-beta; 1.
DR PRINTS: PRO0438; GFCYSKOT.
DR PRINTS: PRO0670; INHIBINB.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KM Follitropin inhibitor; Contrareptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1
FT PROPEP 29 310
FT CHAIN 311 426
FT DISULFID 314 322
FT DISULFID 321 391
FT DISULFID 350 423
FT DISULFID 354 425
FT DISULFID 390 390
FT CARBOHYD 165 165
FT CONFLICT 377 379
SQ SEQUENCE 426 AA; 47442 MW; 201CDEDF9CB6919 CRC64;
Query Match 54.4%; Score 498; DB 1; Length 426;
Best Local Similarity 45.5%; Pred. No. 2,49e-109;
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
Db 306 RRRRGLECDGKVNICCKKQFFVSKDIGNMDWIIASGYHANCCEDECSHIAGTSGSS 365
OY 1 RARRPTCEPATPCPCCRDHYVDFOELGWRWILQEGYQNLNCSQCCPPHLGSPGIA 60
Db 366 LSFHSTVINHYRMGSHSPFANLKCQVPTKLRPSMXYDDGNIIRKDIQNMIVBCCG 425
OY 61 ASFHSAVS-L-LRANNWPASTSCCVPTARRPLSLYLDRNGWVATDVPDMVVEACGC 118
Db 426 S 426
OY 119 S 119

RESULT 12
ID ITHBA_CHICK STANDARD: PRT: 424 AA.
AC P27092; Q90697.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
GN Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=WHITE LEGHORN;
CC Huang J.X.;
CC Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC [2]
CC SEQUENCE FROM N.A.
CC STRAIN=WHITE LEGHORN;
CC MEDLINE: 96380183.
CC Chen C.C., Johnson P.A.;
RT "Molecular cloning of inhibin/activin beta A-subunit complementary RT beta A subunits in the domestic hen.";
RL beta A subunits in the domestic hen.";
RL Biol. Reprod. 54:429-435(1996).
[3]
CC SEQUENCE OF 317-349 FROM N.A.
CC TISSUE=HYPOBLAST;
CC MEDLINE: 91029482.

RA Mitrani E., Ziv T., Thomsen G., Shimoni Y., Melton D.A., Brill A.;
RT "Activin can induce the formation of axial structures and is
RL expressed in the hypoblast of the chick."
Cell 63:495-501(1990).
CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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DR EMBL: U26946; AAA68174.1; -;
DR EMBL: U42377; AAC59738.1; -;
DR EMBL: M61167; AAA48569.1; -;
DR EMBL: M57407; AAA03080.1; -;
DR PIR: B36193; B36193.
DR HSSP: P18075; IBM.
DR PFAM: PF00019; TGF-beta; 1.
DR PFAM: PF00688; TGF-beta; 1.
DR PRINTS: PR00438; GRCYSKNOT.
DR PRINTS: PR00670; INHIBINB.
DR PROSITE: PS00250; TGF_BETA_1; FALSE NEG.
KW Follitropin inhibitor; Contrareptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 26
FT PROPEP 29 308
FT CHAIN 309 424
FT DISULFID 312 320
FT DISULFID 319 389
FT DISULFID 348 421
FT DISULFID 352 423
FT DISULFID 388 388
FT CARBOHYD 165 165
FT CONFLICT 33 33
FT CONFLICT 87 87
FT CONFLICT 188 188
FT CONFLICT 213 213
FT CONFLICT 235 235
FT CONFLICT 307 307
FT CONFLICT 350 350
SQ SEQUENCE 424 AA; 47574 MW; 96E158FE119E1D69 CRC64;
Query Match 52.1%; Score 477; DB 1; Length 424;
Best Local Similarity 43.8%; Pred. No. 2.75e-103;
Matches 53; Conservative 32; Mismatches 34; Indels 2; Gaps 2;

DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN).
GN INHIB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archaeoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CC [1]
CC SEQUENCE FROM N.A.
CC TISSUE-FOLLICLE.
CC Klinger H., Haleschek-Wiener J., Wohlrab B.K., Kuchler K., Wohlrab F.;
CC Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC [2]
CC SEQUENCE FROM N.A.
CC STRAIN-WHITE LEGHORN; TISSUE-OVARY;
CC Hecht D.J., Davis A.J., Ryan I.M., Johnson P.A.;
CC Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC [3]
CC SEQUENCE OF 311-381 FROM N.A.
CC MEDLINE: 91029482.
RA Mitrani E., Ziv T., Thomsen G., Shimoni Y., Melton D.A., Brill A.;
RT "Activin can induce the formation of axial structures and is expressed
RL in the hypoblast of the chick."
Cell 63:495-501(1990).
CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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DR EMBL: Z71594; CAA96248.1; -;
DR EMBL: AF05478; AAC14187.1; -;
DR EMBL: M61166; AAA48568.1; -;
DR EMBL: M57408; AAA03079.1; -;
DR HSSP: P18075; IBM.
DR PFAM: PF00019; TGF-beta; 1.
DR PFAM: PF00688; TGF-beta; 1.
DR PRINTS: PR00438; GRCYSKNOT.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Follitropin inhibitor; Contrareptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 25
FT PROPEP 26 276
FT CHAIN 277 391
FT DISULFID 280 288
FT DISULFID 287 356
FT DISULFID 316 388
FT DISULFID 320 390
FT DISULFID 355 355
FT CARBOHYD 77 77
FT CONFLICT 30 30
SQ SEQUENCE 391 AA; 43608 MW; 060017BF337FAF6C CRC64;
Query Match 51.7%; Score 474; DB 1; Length 391;
Best Local Similarity 49.2%; Pred. No. 2.00e-102;
Matches 59; Conservative 24; Mismatches 36; Indels 1; Gaps 1;

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Query Match          51.4% ; Score 471; DB 1; Length 255;
Best Local Similarity 48.3% ; Pred. No. 1,45e-101;
Matches             58; Conservative      27; Mismatches 34; Indels   1; Gaps    1;

Db              136 RIKRGLCDGRTSLCCROQFIDFLPLISMDNMIAPGYGNATCEGSPAYLAGVPSA 195
               1 1 1 1 : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy              1 RARRPTFCPEAPLPCLCRDHYVDFOELGRDMILQPEGYQLNCSCGCCPHLNGSPGIA 60
               | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db              196 SPSFTAVVNOYRMNGJPGVPVNSCIPITLSMSMLYEDDENITYKRDPMYIEBCGA 255
               : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy              61 ASFSHAFSLSKANNPMPAST -SCCPYIARRLSLTLYIDHGNNVKTDVPMVEACGS 119
               | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT         15
ID             IHBB_PIG                STANDARD;           PRT;       349 AA.
AC             P04088;
DT             01-NOV-1986 (Rel. 03, Created)
DI             01-NOV-1986 (Rel. 03, Last sequence update)
DT             15-JUL-1998 (Rel. 36, Last annotation update)
DE             INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) (FRAGMENT).
GN             INHB.
OS             Sus scrofa (Pig).
OC             Euxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC             Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN             [1]
RP             SEQUENCE FROM N.A.
RC             TISSUE-OVARIAN FOLLICULAR FLUID;
RX             MEDLINE; 86092207.
RA             Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,
RT             Guillaume R., Niail H., Seeburg P.H.;
RT             *Complementary DNA sequences of ovarian follicular fluid inhibin show
RT             precursor structure and homology with transforming growth
RT             factor-beta." ;
RT             Nature 318:659-663(1985).
RN             [2]
RP             SEQUENCE OF 235-249.
RX             MEDLINE; 92355604.
RA             Nakamura T., Asashima M., Eto Y., Takio K., Uchiyama H., Moriya N.,
RA             Arizumi T., Yoshino T., Sugino K., Titani K., Sugino H.;
RT             J.Biol.Chem. 267:16385-16389(1992).
CC             -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INHIBITS THE
CC             SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC             ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC             IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC             -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC             INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC             INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC             ACTIVIN AB IS A DIMER OF BETA-A.
CC             -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
-----
CC             CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC             between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC             the European Bioinformatics Institute. There are no restrictions on its
CC             use by non-profit institutions as long as its content is in no way
CC             modified and this statement is not removed. Usage by and for commercial
CC             entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC             or send an email to license@isb-sib.ch).
-----
DR             EMBL: X03267; CAJ27021.1; -.
DR             PTR, A01394; WFGGB.
DR             DR HSSP: P18075; IBMP.
DR             DR PFAM: PF00019; TGF-beta.1.
DR             DR Pfam: PF00688; TGF-beta_propeptide.1.
DR             DR PROSITE: PS00250; TGF_beta.1; 1.
KM             Follitropin inhibitor; Contrareptive; Hormone; Glycoprotein.
FT             NON TER                      1
FT             PROPEP                       <1
FT             CHAIN                        234
FT             CHAIN                        349
FT             DISULFID                     238
FT             DISULFID                     246
FT             DISULFID                     245
FT             DISULFID                     314
BY             INHIBIN BETA B CHAIN.
BT             BY SIMILARITY.
BT             BY SIMILARITY.
```

Thu Aug 17 10:22:13 2000

US-08-765-662-12.rsp

Page 10

SEQUENCE	349 AA:	39354 MW:	C57LEA91ADA5DE77 CRC64:
FT DISULFID	274	346	BY SIMILARITY.
FT DISULFID	278	348	BY SIMILARITY.
FT DISULFID	313	313	INTERCHAIN (BY SIMILARITY)
FT CARBOHYD	35	35	POTENTIAL.

51.1%; Score 468; DB 1; Length 349;

Query Match	51.1%	Score 468;	DB 1;	Length 349;
Best Local Similarity	48.3%	Pred. No. 1.05e-100;		
Matches	58;	Conservative	25;	Mismatches 36;
			Indels	1;
			Gaps	1;

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D6      290 S$FTAAVNVQYRMGRINPGTVNSCCIPKLTSMMLYEDEYNLYKRDPANNIVEEGCA    349
```

::|::| : ::|| |::|:|::|::|::|::|:

```
D7      61 ASFSISAVFSLTKANNPWAST-SCCVPARARPUSLLYLHDHNGNVAKTDPMPVVEACGCS   119
```

Search completed: Thu Aug 17 10:17:28 2000
Time : 30 secs.

3

 NWRESE
 (TM)

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Search: protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Aug 17 10:17:46 2000; MasPar time 13.47 Seconds
 612.688 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-662-12
 Description: (1-119) from 5929213.pep
 Perfect Score: 916
 Sequence: 1 RARRRTPCEPATPLCCRRD.....NGNVKTDVPMVVEACGCS 119

Scoring table:
 PAM 150
 Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: splrembl12
 1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
 5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
 9:sp.phage 10:sp.plant 11:sp.prodent 12:sp.unclassified
 13:sp.verttebrate 14:sp.virus

Statistics: Mean 39.398; Variance 61.413; scale 0.642
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	630	68.8	351	11	ACTIVIN BETA C.	8.97e-132
2	619	67.6	367	13	ACTIVIN D PRECURSOR.	6.80e-129
3	474	51.7	370	13	ACTIVIN BETA B SUBUNIT	2.67e-91
4	472	51.5	413	13	ACTIVIN BETA-A SUBUNIT	8.69e-91
5	464	50.7	393	13	ACTIVIN BETA B.	9.74e-89
6	439	47.9	138	13	ACTIVIN BETA B PROTEIN	2.36e-82
7	421	46.0	120	13	ACTIVIN BETA A PROTEIN	8.86e-78
8	415	45.3	119	13	ACTIVIN BETA B (FRAGMENT)	2.94e-76
9	397	43.3	104	13	ACTIVIN BETA-B SUBUNIT	1.04e-71
10	387	42.2	102	13	ACTIVIN BETA-A SUBUNIT	3.44e-69
11	386	42.1	102	13	ACTIVIN BETA-B-2 SUBUNIT	6.14e-69
12	385	42.0	102	13	ACTIVIN BETA-B-1 SUBUNIT	1.09e-68
13	382	41.7	361	5	BONE MORPHOGENETIC PRO	6.21e-68
14	362	39.5	365	5	DECAPENTAPLEGIC PROTEI	6.32e-63
15	362	39.5	365	5	CET-1.	6.32e-63
16	357	39.0	289	5	BONE MORPHOGENETIC PRO	1.12e-61
17	353	38.5	204	5	BONE MORPHOGENETIC PRO	1.11e-60
18	352	38.4	400	13	BONE MORPHOGENETIC PRO	1.96e-60
19	352	38.4	400	13	PROTEIN 4.	1.96e-60
20	352	38.4	400	13	BONE GENETIC PROTEIN 4	1.96e-60

Result ID	Query Match	Score	Length	DB	Best Local Similarity	Conservative	Mismatches	Indels	Gaps
21	350	38.2	411	13	0.93108				
22	350	38.2	411	13	0.93369				
23	350	38.2	411	13	0.93753				
24	347	37.9	354	13	0.93753				
25	347	37.9	400	13	0.93107				
26	344	37.6	386	13	0.93109				
27	343	37.4	417	5	0.93707				
28	341	37.2	178	5	0.93211				
29	336	36.7	191	5	0.92468				
30	334	36.5	301	5	0.93790				
31	333	36.4	373	13	0.90723				
32	333	36.4	373	13	0.98950				
33	333	36.4	373	13	0.91643				
34	333	36.4	428	5	0.91613				
35	333	36.4	428	5	0.91613				
36	337	35.7	443	5	0.96851				
37	333	35.3	356	13	0.93139				
38	323	35.3	614	5	0.91720				
39	320	34.9	313	13	0.91403				
40	317	34.6	424	13	0.91613				
41	310	33.8	399	13	0.97573				
42	310	33.8	453	13	0.97573				
43	309	33.7	257	13	0.94203				
44	309	33.7	261	13	0.98660				
45	308	33.6	126	13	0.93573				

ALIGNMENTS

Result ID	Query Match	Score	Length	DB	Best Local Similarity	Conservative	Mismatches	Indels	Gaps
1	68.8%	630	351	11	8.97e-132				
2	67.6%	619	367	13	6.80e-129				
3	51.7%	474	370	13	2.67e-91				
4	51.5%	472	413	13	8.69e-91				
5	50.7%	464	393	13	9.74e-89				
6	47.9%	439	138	13	2.36e-82				
7	46.0%	421	120	13	8.86e-78				
8	45.3%	415	119	13	2.94e-76				
9	43.3%	397	104	13	1.04e-71				
10	42.2%	387	102	13	3.44e-69				
11	42.1%	386	102	13	6.14e-69				
12	42.0%	385	102	13	1.09e-68				
13	41.7%	382	361	5	6.21e-68				
14	39.5%	362	365	5	6.32e-63				
15	39.5%	362	365	5	6.32e-63				
16	39.0%	357	289	5	1.12e-61				
17	38.5%	353	204	5	1.11e-60				
18	38.4%	352	400	13	1.96e-60				
19	38.4%	352	400	13	1.96e-60				
20	38.4%	352	400	13	1.96e-60				

```

DT 01-NOV-1999 (TREMblrel. 12, last annotation update)
DE ACTIVIN D PRECURSOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE; 95275314.
RA ODA S., NISHIMATSU S., MURAKAMI K., UENO N.;
RT "Molecular cloning and functional analysis of a new activin beta
subunit: a dorsal mesoderm-inducing activity in Xenopus."
RL Biochem. Biophys. Res. Commun. 210:581-588(1995).
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; D49543; BAA08494.1; -.
DR HSSP; P18075; IBMF.
DR PROSITE; PS00250; TGF-BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR SIGNAL; Glycoprotein.
SQ CHAIN 1 253 POTENTIAL.
SEQUENCE 367 AA; 41729 MW; E798693F CRC32;

Query Match 67.6%; Score 619; DB 13; Length 367;
Best Local Similarity 62.2%; Pred. No. 6,80e-129;
Matches 74; Conservative 25; Mismatches 20; Indels 0; Gaps 0;

DB 249 HATKRSINDODNSLCCCKRDYVDKDGMDWIKPEGYOINCMGLCPHMGAGPMA 308
OY 1 RARRPTCEPATPLCCRRDHYVDFOELGWRDWIIQPGYOLNCSGCCPHLGGSPGIA 60

DB 309 ASFHNTVLNKKANNIQTAVNSCCVPTKRRLPLMLFDRNNNNVKTIDADMIVEACGS 367
OY 61 ASHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLDHNGNVKTDVDMVVEACGS 119

RESULT 3
ID 091350 PRELIMINARY; PRT; 370 AA.
AC 091350;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, last annotation update)
DE ACTIVIN BETA B SUBUNIT.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE; 93273083.
RA DOHRMANN C.E., HEMMATI-BRIVANLOU A., THOMSEN G.H., FIELDS A.,
RA WOLF T.M., MELTON D.A.;
RT "Expression of activin mRNA during early development in Xenopus
laevis."
RL Dev. Biol. 157:474-483(1993).
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; S61773; AAB26863.1; -.
DR HSSP; P18075; IBMF.
DR PROSITE; PS00250; TGF-BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR Glycoprotein.
SQ SEQUENCE 370 AA; 41678 MW; 58CE42C9 CRC32;

Query Match 51.7%; Score 474; DB 13; Length 370;
Best Local Similarity 48.3%; Pred. No. 2,67e-91;
Matches 58; Conservative 25; Mismatches 36; Indels 1; Gaps 1;

DB 251 RIRRGLECDHTNLCRCQGFYIDFRLGNWDWIIAPAGYGNVCEGSPAYLAGVGS 310
OY 1 RARRPTCEPATPLCCRRDHYVDFOELGWRDWIIQPGYOLNCSGCCPHLGGSPGIA 60
OY 61 ASHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLDHNGNVKTDVDMVVEACGS 119

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OY 1 RARRPTCEPATPLCCRRDHYVDFOELGWRDWIIQPGYOLNCSGCCPHLGGSPGIA 60
DB 311 SSFHTAVNQRNRGLNPGVNSCCIPETKLSMSMIFPDEXNIVKRDVPMNIVECGCA 370
OY 61 ASHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLDHNGNVKTDVDMVVEACGS 119

RESULT 4
ID 098660 PRELIMINARY; PRT; 413 AA.
AC 098660;
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, last annotation update)
DE ACTIVIN BETA-A SUBUNIT.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Caudata; Salamandroidae; Salamandridae; Cynops.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE; 96295508.
RA YAMAMOTO T., NAKAYAMA Y., ABE S.;
RT "Expression of activin beta subunit genes in Sertoli cells of newt
testes."
RL Biochem. Biophys. Res. Commun. 224:451-456(1996).
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; D84516; BAA12693.1; -.
DR HSSP; P18075; IBMF.
DR PROSITE; PS00250; TGF-BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
DR PFAM; PF00688; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00670; INHIBINB.
DR Glycoprotein.
SQ SEQUENCE 413 AA; 46303 MW; 77A4302D CRC32;

Query Match 51.5%; Score 472; DB 13; Length 413;
Best Local Similarity 43.0%; Pred. No. 8,69e-91;
Matches 52; Conservative 33; Mismatches 34; Indels 2; Gaps 1;

DB 293 RRRKRLCEDGKVSIOCKQKQFYVSKFDIGMSDWIAPPGYIANTYCEGCPMYITGSSG 352
OY 1 RARRPTCEPATPLCCRRDHYVDFOELGWRDWIIQPGYOLNCSGCCPHLGGSPGIA 60
OY 61 ASHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLDHNGNVKTDVDMVVEACGC 118
DB 353 PSFHAVINQYMRGVSPTSVKSCVPTKLRMSMLYYDDGONIKKIDIONMVVEECGC 412
OY 61 ASHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLDHNGNVKTDVDMVVEACGC 118
DB 413 S 413
OY 119 S 119

RESULT 5
ID 090261 PRELIMINARY; PRT; 393 AA.
AC 090261;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, last annotation update)
DE ACTIVIN BETA B.
GN ZACTBB OR ZACTBETAB.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE; 95011355.
RA WITTBRODT J., FREDERIC R.M.;
RT "Disruption of mesoderm and axis formation in fish by ectopic
expression of activin variants: the role of maternal activin."
RL Genes Dev. 8:1448-1462(1994).
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.

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DR EMBL: X76051; CAA53636.1; -.
DR HSSP; P18075; 1BMP.
DR ZFIN; ZDB-GENE-950415-2; zactbDb.
DR PROSITE; PS00250; TGF_BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
DR PFAM; PF00688; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR GLYCOPROTEIN.
KW SEQUENCE
SQ SEQUENCE 393 AA; 43850 MW; 14DE189C CRC32;

Query Match
Best Local Similarity 47.9%; Score 464; DB 13; Length 393;
Matches 58; Conservative 24; Mismatches 37; Indels 2; Gaps 2;

Db 273 RIRKRGLEDGNNGLCCROQFYIDFRLIGNDWIIAPAGYGNCEGSCPAYMAGVPGS 332
1 RARRRPTCEPATP-LCCRRDHYVDFOELGMRDWILOPEGYQNTCSGCGPPHLAGSPGI 59
333 ASFTFAVNOYRMGMSPGNSVNSCIPKLTSMILYFDDENIYKRDVPMNIVEEGC 392
60 AASFHSAVSLKANNPWPAST-SCCVPTARRPLSLYLIDHNGNVKTDVPMVVEACGC 118
393 A 393
119 S 119

RESULT 6
ID 09M6T9 PRELIMINARY; PRT; 138 AA.
AC 09M6T9;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
GN ACTIVIN BETA B PROTEIN (FRAGMENT).
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RA RODAWAY A., TAKEDA H., KOSHIDA S., PRICE B.M., SMITH J.C., PATIENT R.,
RA HOLDER N.;
RT Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
RL -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
EMBL: AJ238981; CABA3092.1; -.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
FT NON_TER 1 1
FT SEQUENCE 138 AA; 15263 MW; 9055EB6D CRC32;

Query Match
Best Local Similarity 47.9%; Score 439; DB 13; Length 138;
Matches 55; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

Db 21 CDGNGGLCCROQFYIDFRLIGNDWIIAPAGYGNCEGSCPAYMAGVPGSASFTAV 80
1 RARRRPTCEPATP-LCCRRDHYVDFOELGMRDWILOPEGYQNTCSGCGPPHLAGSPGIASFHSAV 67
9 CBPAIP-LCCRRDHYVDFOELGMRDWILOPEGYQNTCSGCGPPHLAGSPGIASFHSAV 67
81 VVOYRMGMSPGNSVNSCIPKLTSMILYFDDENIYKRDVPMNIVEEGC 132
68 FSLKANNPWPAST-SCCVPTARRPLSLYLIDHNGNVKTDVPMVVEACGC 118

RESULT 7
ID 09M6T8 PRELIMINARY; PRT; 120 AA.
AC 09M6T8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE ACTIVIN BETA A PROTEIN (FRAGMENT).

GN ACTIVIN BETA A.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RA RODAWAY A., TAKEDA H., KOSHIDA S., PRICE B.M., SMITH J.C., PATIENT R.,
RA HOLDER N.;
RT Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
RL -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
EMBL: AJ238980; CABA3091.1; -.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
FT NON_TER 1 1
FT SEQUENCE 120 AA; 13583 MW; B34108BB CRC32;

Query Match
Best Local Similarity 46.0%; Score 421; DB 13; Length 120;
Matches 46; Conservative 34; Mismatches 29; Indels 2; Gaps 2;

Db 4 CDGARVCKRQFYVNFKDIGNDWIIAPAGYGNCEGSCPAYMAGVPGS 63
9 CEPATPLCCRRDHYVDFOELGMRDWILOPEGYQNTCSGCGPPHLAGSPGIASFHSAV 68
64 SHYRIGYSPFTNIKSCVPTARRPLSLYLIDHNGNVKTDVPMVVEACGC 117
69 S-L-LKANNPWPASTSCCVPTARRPLSLYLIDHNGNVKTDVPMVVEACGC 117

RESULT 8
ID 042125 PRELIMINARY; PRT; 119 AA.
AC 042125;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
GN ACTIVIN BETA B (FRAGMENT).
OS Pagrus major (Red sea bream) (Chrysophrys major).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Perciformes;
OC Perciformes; Percoidae; Sparidae; Chrysophrys.
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-OVERY;
RA SAKAKIDA Y., KASAHARA M., INABA K.;
RL Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
EMBL: AB06786; BAA22570.1; -.
DR HSSP; P18075; 1BMP.
DR PROSITE; PS00250; TGF_BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
KW Glycoprotein.
FT NON_TER 1 1
FT SEQUENCE 119 AA; 13455 MW; 3BBD4F6B CRC32;

Query Match
Best Local Similarity 45.3%; Score 415; DB 13; Length 119;
Matches 52; Conservative 24; Mismatches 33; Indels 1; Gaps 1;

Db 10 RIRKRGLEDGSSSLCCROQFYIDFRLIGNDWIIAPAGYGNCEGSCPAYMAGVPGSA 69
1 RARRRPTCEPATP-LCCRRDHYVDFOELGMRDWILOPEGYQNTCSGCGPPHLAGSPGI 60
70 SSFTFAVNOYRMGMSPGNSVNSCIPKLTSMILYFDDENIYKRDV 119
61 AASFHSAVSLKANNPWPAST-SCCVPTARRPLSLYLIDHNGNVKTDV 109

RESULT 9
ID 098861 PRELIMINARY; PRT; 104 AA.
AC 098861;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE ACTIVIN BETA A PROTEIN (FRAGMENT).
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AC 09861;
DT 01-FEB-1997 (TREMBLER. 02, Created)
DT 01-FEB-1997 (TREMBLER. 02, Last sequence update)
DT 01-NOV-1999 (TREMBLER. 12, Last annotation update)
DE ACTIVIN BETA-B SUBUNIT (FRAGMENT).
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RX MEDLINE: 96295508.
RA YAMAMOTO T., NAKAYAMA Y., ABE S.;
RT "Expression of activin beta subunit genes in Sertoli cells of newt
  testes.";
RL Biochem. Biophys. Res. Commun. 224:451-456(1996).
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL: D84517; BAI12694.1; -.
DR HSSP: P18075; IBM.
DR PROSITE: PS00250; TGF-BETA: 1.
DE PPM: PF00019; TGF-beta: 1.
DE Glycoprotein.
FT NON_TER 1
FT SEQUENCE 104 AA: 11676 MW; 74527D82 CRC32;
Query Match 43.3%; Score 397; DB 13; Length 104;
Best Local Similarity 50.0%; Pred. No. 1,04e-71;
Matches 51; Conservative 21; Mismatches 29; Indels 1; Gaps 1;

Db 3 TNLCCROGFYIDFRLIGNMDIIPAGYFGNYCEGSCPAYLAGVGSASFHTAVNOYR 62
1 | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 13 TPLCCRRDHYVDFQELGMDWILQPEGYQLNYCSGQCPHLGSPGIAASHFASFLK 72
1 | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

Db 63 MRGLNPGVNSCIPYTKLSTMSMLYFDEYNIVKRDVPMNV 104
1 | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 73 ANNPAPAST-SCVPTARRPLSLYLDHNGNVKTDVPMV 113
1 | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 10
ID 090390; PRELIMINARY; PRT; 102 AA.
AC 090390;
DT 01-NOV-1996 (TREMBLER. 01, Created)
DT 01-NOV-1996 (TREMBLER. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLER. 12, Last annotation update)
DE ACTIVIN BETA-A SUBUNIT (FRAGMENT).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Cyprinidae; Carassius.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE: 93290666.
RA GE W., GALLIN W.J., STROBECK C., PETER R.E.;
RT "Cloning and sequencing of goldfish activin subunit genes: strong
  structural conservation during vertebrate evolution.";
RL Biochem. Biophys. Res. Commun. 193:711-717(1993).
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DE EMBL: L15339; AAA49162.1; -.
DR HSSP: P18075; IBM.
DR PROSITE: PS00250; TGF-BETA: 1.
DE PPM: PF00019; TGF-beta: 1.
DE Glycoprotein.
FT NON_TER 1
FT SEQUENCE 102 AA: 11849 MW; 4B6A0E7C CRC32;
Query Match 42.2%; Score 387; DB 13; Length 102;
Best Local Similarity 43.4%; Pred. No. 3,44e-69;
Matches 43; Conservative 29; Mismatches 25; Indels 2; Gaps 2;

Db 4 VCCRRQFYVNFKIDGMSDIIAPSGIYHANYCEBGDCPSHVASTIGSALSFHTVINYMR 63
1 | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
1
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QY 15 LCCRRDHYVDFQELGMDWILQPEGYQLNYCSGQCPHLGSPGIAASHFASFLK 72
1 | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 64 GYSPFNKSCVPTARRPLSLYLDHNGNVKTDVPM 110
1 | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 73 ANNPAPAST-SCVPTARRPLSLYLDHNGNVKTDVPM 111
1 | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 11
ID 090389; PRELIMINARY; PRT; 102 AA.
AC 090389;
DT 01-NOV-1996 (TREMBLER. 01, Created)
DT 01-NOV-1996 (TREMBLER. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLER. 12, Last annotation update)
DE ACTIVIN BETA-B-2 SUBUNIT (FRAGMENT).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Cyprinidae; Carassius.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE: 93290666.
RA GE W., GALLIN W.J., STROBECK C., PETER R.E.;
RT "Cloning and sequencing of goldfish activin subunit genes: strong
  structural conservation during vertebrate evolution.";
RL Biochem. Biophys. Res. Commun. 193:711-717(1993).
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DE EMBL: L15340; AAA49160.1; -.
DR HSSP: P18075; IBM.
DR PROSITE: PS00250; TGF-BETA: 1.

Query Match 42.1%; Score 386; DB 13; Length 102;
Best Local Similarity 51.0%; Pred. No. 6,14e-69;
Matches 50; Conservative 19; Mismatches 28; Indels 1; Gaps 1;

Db 5 LCCRRQFYVDFQELGMDWILQPEGYQLNYCSGQCPHLGSPGIAASHFASFLK 74
1 | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 15 LCCRRDHYVDFQELGMDWILQPEGYQLNYCSGQCPHLGSPGIAASHFASFLK 74
1 | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

Db 65 GMSPGVNSCIPYTKLSTMSMLYFDEYNIVKRDVPM 102
1 | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 75 NNPAPAST-SCVPTARRPLSLYLDHNGNVKTDVPM 111
1 | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 12
ID 090388; PRELIMINARY; PRT; 102 AA.
AC 090388;
DT 01-NOV-1996 (TREMBLER. 01, Created)
DT 01-NOV-1996 (TREMBLER. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLER. 12, Last annotation update)
DE ACTIVIN BETA-B-1 SUBUNIT (FRAGMENT).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Cyprinidae; Carassius.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE: 93290666.
RA GE W., GALLIN W.J., STROBECK C., PETER R.E.;
RT "Cloning and sequencing of goldfish activin subunit genes: strong
  structural conservation during vertebrate evolution.";
RL Biochem. Biophys. Res. Commun. 193:711-717(1993).
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DE EMBL: L15340; AAA49160.1; -.
DR HSSP: P18075; IBM.
DR PROSITE: PS00250; TGF-BETA: 1.
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